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KEYWORDS

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143358 Sequence 1		I32051 Sequence 1	AX838364 Sequence	AX817767 Sequence		CQ854904 Sequence	CQ854905 Sequence	AR230727 Sequence	AR102229 Sequence	AR091536 Sequence	AX084519 Sequence	AR403724 Sequence	AX084516 Sequence		AX084505 Sequence	AX084517 Sequence	AX084504 Sequence	AF534906 Human ade	J01917 Adenovirus	AX770200 Sequence	BD268237 Adenoviru	BD021943 Packaging			BD021940 Packaging

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Perricaudet,M., Akusjarvi,G., Virtanen,A. and Pettersson,U. Structure of two spliced mRNAs from the transforming region human subgroup C adenoviruses
Nature 281 (5733), 694-696 (1979)
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Hearing, P. and Shenk, T.
Hearing, P. analysis of the nucleotide
Functional analysis of the region EIA
site for adenovirus type 5 region EIA
site for 167 (4), 809-822 (1983)
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The 2.2 kb E1b mRNA of human Ad12 and Ad5 codes for two tumor antigens starting at different AUG triplets
Cell 27 (1 Pt 2), 121-131 (1981)
                                             14 (bases 1 to 66)
Nagata, K., Guggenheimer, R.A. and Hurwitz, J.
Specific binding of a cellular DNA replication protein to origin of replication of adenovirus DNA
Proc. Natl. Acad. Sci. U.S.A. 80 (20), 6177-6181 (1983)
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Fowlkes, D.M. and Shenk, T.

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Cell 22 (2 Pt 2), 405-413 (1980)
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7 (bases 2804 to 4125)
Maat,J., van Beveren,C.P. and van Ormondt,H.
Maat,J., van Beveren,G.P. and van Ormondt,H.
The nucleotide sequence of adenovirus type 5 early region E1: the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Appendix d: nucleotide sequences, transcription and translation analyses, and restriction endonuclease cleavage maps of group-c
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TUMOR VIRUSES: 937-1002;
d Spring Harbor Laboratory
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the main adenovirus 2 entry).

large amounts of small rnas are produced from the vai and vaii genes late in development for unknown reasons. [5] and [6] demonstrate that vai gene activity influences vaii expression; that the 5' flank affects the start site of the rna but that an intragenic promoter (bases 10626 to 10690 below) determines whether the rna is actually produced; and that there is striking similarity between this rna and trna.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as some basis for the annotation of sites. the differences betweer cad2> and cad5> are too many to report herein, however a printout of those is available upon request for grebank. The map coordinates in the sites presume 360 bases per map unit although there are approximately 115 sequence differences between the two strains over this region, no site difference exceeds 0.02% by this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the sequence represents the early mrna transcripts ela and elb and the intermediate mrna transcript ix, all of which are transcribed rightwardly off the r-strand; the iva2 and e2b mrnas which are transcribed leftwardly off the l-strand ((indicated by '(c)' and 'comp strand' below); and the 5 end of the 28 kb major late mrna the cap sites and possible promoter sequences for these are summarized in the following table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             major 6049 tataaaa at bases 6018-6024 [10] with ad2, not all the transcripts from this region have been characterized at the sequence level. the nine proteins given in features table below are not the only possible gene products (so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tatttata at bases 468-475 [6] elb tatataa at bases 1672-1678[6] ix 582 tatataa at bases 1581-3557 [6] iva2 5838 tacaaa at bases 5979-5974 on the comp strand [10]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence corresponds to bases 1 to 11560 of <ad2>, which serve
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The nucleotide sequence of fragment HindIII-C of human adenovirus type 5 DNA (map posttions 17.1-31.7)
Gene 27 (1), 115-120 (1984)
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/mol_type="genomic DNA"
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499. .1632
/note="primary transcript of EIA region"
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Patent: WO 2004066947-A 3 12-AUG-2004;
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Location/Qualifiers
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1239 TGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAAGACCTACCCGCCGTCCTAA 1298 841 AATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGTCTAGAGAATTGCAATAGTAG 900	Q B	ORGANISM Human adenovirus C ORGANISM Human adenovirus C Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.	SO
781 TGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAAGACCTACCCGCCGTCCTAA 840	Qy	.1 GI:1318591	S E A
721 TITTACAGTTTIGIGGTTTAAAGAATTTIGIATIGIGATTITTTAAAAAGGTCCTGIGIC 780 	Db Qy	AX084506 AX084506 33699 bp DNA linear PAT 28-FEB-2001 DEFINITION Sequence 3 from Patent WO0104282.	DECAR
1119 GAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTGGTAATTTTTTTT	B &	2409 C100C	9 5
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ATGATTTAGACGTGACGGCCCCGAAGATCCCAACGAGGAGGCGGTTTCGCAGATTTTTC
                           CGTGTAGTGTATTTATACCCCGGTGAGTTCCTCAAGAGGCCACTCTTGAGTGCCAGCGAGT
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/mol_type="unassigned DNA"
/db_xref="taxon:129951"
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		81 39	da VQ
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		781 TGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAAGACCTACCCGCCGTCCTAA 840	å Š
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	Q B \$	661 GAAAATTATGGGCAGTGGTGATAGAGTGGTGGGTTTGGTGTGAATTTTTTTT	dg VQ
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	£ £ \$	421 TGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATCGATC	B 8
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Submitted (09-JUL-2003) Process Sciences, Canji Inc., Schering-Plough Corporation, 3525 John Hopkins Court, San 92121, USA
                                                                                                                                                                                                                                                                                                                                                            Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadeńovirus.

1 (bases 1 to 35934)

MCAllister B. 7.

CHORSTON B. 7.
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2 (bases 1 to 35934)
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KUCYLADAQGEDRORFSTSRTSLKRTLASAQPGAHPFTVTQTTLTRTLRFWKMMTLARL
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rlriqqagfkmvllstirrlktayfayiisstsarnnpdrrplppatulslecdem
ldaflerfsdpudadslrslgggvptqqllrcivsavslphgspppthnrdmtggufq
ldrprengraytetmrrrrggwfq
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TTLTYETVSGTPLETAASAAASAAATARGIVTDFAFLSPLASSAASRSSARDDKLTA
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complement(8583. .10544)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="for E2B IVa2 mRNA" 6018. .6024
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complement (5428. .5705)
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YSRVWNEGGLNAFSQLMAR I SNDLAATVERAGRGDLQEEE I EQFMAE I AYQDNSGDVÇ
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/replace="g"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="putative precursor"
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Best Local :
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                             CAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGCATGTTTGTCTACAGTAAGT
                                                                                                                                                                                                                                                                                                                       CCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTACTCACTTTTCCGCCGGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGATTTAGACGTGACGGCCCCCGAAGATCCCCAACGAGGAGGCGGTTTCGCAGATTTTTC
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CAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGCATGTTTGTCTACAGTAAGT
                                                                                              TGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCACCGGAGGAATACGGGGGGACC
                                                                                                                                                 CTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAGGAGTTTGTGTTAGATTATG
                                                                                                                                                                                   CCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCCGAGCAGCCGGAGCAGAGAGCCT
                                                                                                                                                                                                                                                                                                                                                                         CCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTACTCACTTTTCCGCCGGCGC
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ADDDYEPPRRARRYLDLEEGEGLARLGAPS PERFIPRYQLKRDTREAYVPRONLFRDR 
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EQTVNQEINFOKSFNNHVRTLVAREBVAIGLMHLMDFVSALEONPNSKPLMAQLFLIV 
EQTVNQEINFOKSFNNHVRTLVAREBVAIGLMHLMDFVSALEONPNSKPLMAQLFLIV 
OHSRDNEAFROALLNIVEPEGRWLLDLINILOSIVVORRSLSLAKVVAAINYSWLSLG 
KFYARKIXHTFYYPILKEVKKIEGFVRMALKYUTLSDDLEVVERNERLHKAVSVSKRRE 
LSDRELMHSLQRALAGTGSGDREAESYFDAGADLRWAPSRRALEAAGAGPGLAVAPAR
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8783
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ARGADVPLPPLPAGPEPPLPPGARPRHRF"
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/replace="c"
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/db_xref="GI:33465839"
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Pred. No. 0;
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2019 ATGGAGCGAAGAAACCCATCTGAGCGGGGGGTACCTGCTGGATTTTCTGGCCATGCATCT 2078	Db	Qy 481 CTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAGGAGTTTGTGTTAGATTATG 540	. ق
	dd d	Qy 421 TGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAAGTGATCGATC	유 왕
	Q D b	QY 361 CCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCGAGCAGAGCAGAGAGCCT 420	D Qy
	od od i	QY 301 CCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTACTCACTTTTCCGCCGGCGC 360	4G Ab
1321 CAGTACCTCTTGGTTTTGGAGGTTTCTGTGGGGCTTCATCCCAGGCAAAGTTAGTCTGCAG 1380 1779 CAGTACCTCTTGGTTTTGGAGGTTTCTGTGGGGCTCATCCCAGGCAAAGTTAGTCTGCAG 1838 1779 CAGTACCTCTTGGTTTTGGAGGTTTCTGTGGGGCTCATCCCAGGCAAAGTTAGTCTGCAG 1838 1381 AATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTTTGAAATCCTGTGGTGAGCTGTT 1440	ס מ פע	QY 241 ATGATTTAGACGTGACGGCCCCCGAAGATCCCCAACGAGGAGGCGGTTTCGCAGATTTTTC 300	Qy Qy
GGCTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGCGTAACTTGCTGGAACAGAGCTCTAA	9d 4d	QY 181 TACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCACCTACCCTACCCTTCACGAACTGT 240	당 왕
	D 5	QY 121 ACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTGGACCAGCTGATCGAAGAGG 180	유
TGATGTPAGTTPAATAAAGGGTGAGATAATGTTTAACTTGCATGGCGTGTTAAATGGGGC	, p v	Qy 61 AGAGTTTTCTCCTCCGAGGCCGCTCCGACACCGGGACTGAAAATGAGACATATTATCTGCC 120	da VO
GCCATAAGGTGTAAACCTGTGATTGCGTGTTTAACGCCTTTTGTTTTGCTGAATTGAGGCCTTTAACGCCTTTTGTTTTGCTGAATTGAGGCCTTTAACGCCTTTTGTTTTTGCTGAATTGAGGCCATAAGGTGTAAACCTGTGATTGCTGATTGCTGAATTGAGTTAACGCCTTTTGTTTTTGCTGAATTGAGTTAACGCCTTTTGTTTTGCTGAATTGAGTTAACGCCTTTTGTTTTGCTGAATTGAGTTAACGCCTTTTGTTTTGCTGAATTGAGTTAACGCCTTTGTTTAACGCCAGGTGAGTAAACCTGTGAATTGAGTAAACCTGTGAATTGAGTAAAACCTGTGAATTGAGTAAAACCTGTGAATTGAGTAAAAACAAAAAAAA	4 da	OY 1 CGTGTAGTGTATTTATACCCGGTGAGTTCCTCAAGAGGCCACTCTTGAGTGCCAGCGAGT 60	45 55
1021 TATCGAGGACTTGCTTAACGAGCCCGGGCAAACCTTTGGACTTGAAGCGCCCCAG 1080	γ dd γ	Query Match  100.0%; Score 3052; DB 6; Length 35935;  Best Local Similarity 100.0%; Pred. No. 0;  Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	3 m O
	עס	Bource 135935 /organism="unkr/mol_type="unar	ORI
901 TACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTGAGATACACCCGGTGGTCCC 960 	QY	Chamberlain, J.S Adenovirus vect Patent: US 5994	য় চ
841 AATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGTCTAGAGAATGCAATAGTAG 900 	Qy Db	DEFEDENCE 1 (hases 1 to 35035)	SOL
781 TGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAAGACCTACCCGCCGTCCTAA 840	Qy Db	ON Sequence 1 from patent US 5994132.  N AR091533 GI:10018288	VER
721 TTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTTTTTAAAAGGTCCTGTGTC 780	Qy Db	T 6	RES ARC
661 GAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTGGTAATTTTTTTT	Qy Db	Oy 3001 CTGGCCTGCACCCGCGCTGAGTTTGGCTCTAGCGATGAAGATACAGATTGAG 3052	वत ठे
601 CAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGCATGTTTGTCTACAGTAAGT 660 	Qy	Qy 2941 ATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGAGGCCGGATCACTTGGTG 3000	B 8
541 TGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCACCGGAGGAATACGGGGGACC 600	QY	Qy 2881 GTGCTGAGGTACGATGAGACCCGCACCAGGTGCAGACCCTGCGAGTGTGGCGGTAAACAT 2940	B &
939 CTGGCTTTCCACCCAGTGACGACGAGGAGGATGAAGAGGGTGAGGAGTTTGTGTTAAGATTATG 998	 Db	Db 3279 GAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTTTGACATGACCATGAAGATCTGGAAG 3338	ф

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Patent: US 6083750-A 1 04-JUL-2000;
Location/Qualifiers
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Unclassified.
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Chamberlain, J.S. and Kumar-Singh, R.
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AGGCCAGATIGCAAGIACAAGATCAGCAAACTIGIAAATATCAGGAATTGTTGCTACATT AGGCCAGATTGCAAGTACAAGATCAGCAAACTTGTAAATATCAGGAATTGTTGCTACATT	B &	1021 TATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACTTGAGCTGTAAACGCCCCAG 1080	90 VQ
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GALAALACCOACUSAGAACCCGAGAGAGCCCTGGACCCCTCGGGAATGAATGTTTTTACAGGTG	Q B &	601 CAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGCATGTTTGTCTACAGTAAGT 660	dg VQ
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8	B 8	D 49	g Q	Query Match Best Local S Matches 3052	sourc ORIGIN	AUTHORS TITLE JOURNAL FEATURES	SOURCE ORGANIS	DEFINITION ACCESSION VERSION KEYWORDS	RESULT 8 AR116313 LOCUS	g 49	gg Qy	8 8	gg dy	B 8	B &	8 8	B &	g
81 TACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCACCTACCCTTCACGAACTGT 24	121 ACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTGGACCAGCTGATCGAAGAGG 180	61 AGAGTTTTCTCCTCCGAGCCGCTCCGACACCGGGACTGAAAATGAGACATATTATCTGCC 120	1 CGTGTAGTGTATTTATACCCGGTGAGTTCCTCAAGAGGCCACTCTTGAGTGCCAGCGAGT 60	4 Watch 100.0%; Score 3052; DB 6; Length 35935; Cal Similarity 100.0%; Pred. No. 0; B 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	o	Imler,JL., Wehtali,M. and Pavirani,A.  Defective adenoviruses and corresponding complementation lines  Left: US 6133028-A 43 17-OCT-2000;  Location/Qualifiers	Unknown. W Unknown. Unclassified. 1 (bases 1 to 1995)	Sequence 43 from patent US 6133028. AR116313 AR116313.1 GI:14096635	35935 b	3001 CTGGCCTGCACCCGCGCTGAGTTTGGCTCTAGCGATGAAGATACAGATTGAG 3052	2941 ATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGAGCTGAGGCCCGATCACTTGGTG 3000	2881 GTGCTGAGGTACGATGAGACCCGCACCAGGTGCAGACCCTGCGAGTGTGGCGGTAAA¢AT 2940 	2821 GAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTTTGACATGACCATGAAGATCTGGAAG 2880	2761 AGGGGGGTGTTCCTACCTACCATGCAATTTGAGTCACACTAAGATATTGCTTGAGCCC 2820	2701 GCCTGGCCAGTGTTTGAGCATAACATACTGACCCGCTGTTCCTTGCATTTTGGGTAACAGG 2760	2641 TGCTCGGACGGCAACTGTCACCTGCTGAAGACCATTCACGTAGCCAGCC	2581 GTGATTAAGCATAACATGGTATGTGGCAACTGCGAGGACAGGGCCTCTCAGATGCTGACC 2640	2979 AGGGTGCGCCACAATGTGGCCTCCGACTGTGGTTGCTTCATGCTAGTGAAAAGCGTGGCT 3038
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1261 GGCTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGCGTAACTTGCTGGAACAGAGCTCTAA	1201 GGGGCTTAAAGGGTAFATAATGCGCCGTGGGCTAATCTTGGTTACATCTGACCTCATGGA	99	39	21 79	961 GCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGCGTCGCCAGGCTGTGGAATG 	901 TACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTGAGATACACCCGGTGGTCCC	841 AATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGTCTAGAGAATGCAATAGTAG	781 TGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAAGACCTACCCGCCGTCCTAA	721 TTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTTTTTTAAAAGGTCCTGTGTC	661 GAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTGTGGTAATTTTTT	601 CAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGCATGTTTGTCTACAGTAAGT	541 TGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCACCGGAGGAATACGGGGGGACC	481 CTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAGGAGTTTGTGTTAGATTATG	421 TGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATCGATC	361 CCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCGAGCAGAGCCGGAGCAGAGAGCCT	301 CCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTACTCACTTTTCCGCCGGCGC	241 ATGATTTAGACGTGACGGCCCCGAAGATCCCAACGAGGAGGCGGTTTCGCAGATTTTTC	639 TACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCACCTACCCTTCACGAACTGT

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                                                                  Hu,F. and Wu,B.

Therapy for primary and metastatic cancers
Patent: WO 2004066947-A 4 12-AUG-2004;
Shanghai Sunway Biotech Co Ltd (CN)
Location/Qualifiers
                                                                                                                                               unidentified unidentified Viruses; dsDN
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Sequence 4 1
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/db_xref="taxon:10535"
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Similarity 100.0%; F
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CGTGTAGTGTATTTATACCCCGGTGAGTTCCTCAAGAGGCCACTCTTGAGTGCCAGCGAGT
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921 TITAGGTIAATGACCAGACACCGTCCTGAGTGTATTACTTTCAACAGATCAAGGATAAT	b by	841 AATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGTCTAGAGAATGCAATAGTAG 900
861 AAGGGGGTAAAGAAGGGAGGCGGGGGCTTCTGAGGCTTACKAGGAAGCTAAGAATCTAGCT	, p &	781 TGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAAGACCTACCCGCCGTCCTAA 840
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321 CAGTACCTCTTGGTTTTGGAGGTTTTCTGTGGGGCTCATCCCAGGCAAAGTTAGTCTGCAG	B &	241 ATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGGAGGCGGTTTCGCAGATTTTTC 300
261 GCTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGCGTAACTTGCTGGAACAGAGCTCTAA 719 GGCTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGCGTAACTTGCTGGAACAGAGCTCTAA	) B (3	181 TACTIGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCACCTACCCTTCACGAACTGT 240
659	) B &	121 ACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTGGACCAGCTGATCGAAGAGG 180
141 TGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACTTGCATGGCGTGTTAAATGGGGC	Qy Db	AGAGTTTTCTCCTCCGAGGCCGCTCCGACACCGGGACTGAAAATGAGACATATTATCTGCC
	_	4.59 CGTGTBAGTGTBATTATBACCCGGTGBAGTGTGTGTGBAGAGGGCGCGTGTGTGAGGTGAG

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Chamberlain, J.S., Amalfitano, A., Har
Hartigan-O'Connor, D.J.
Helper adenovirus vectors
Patent: US 6451596-A 1 17-SEP-2002;
Location/Qualifiers
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RESULT 11 AX451988 LOCUS AX451988 DEFINITION Sequence 1 from Patent WO0244393. ACCESSION AX451988 .	Db 3399 ATTAGGAACCAGCCTGTGATGCTGGATGTGACCAGGAGCTGAGGCCCGATCACTTGGTG 3458  Qy 3001 CTGGCCTGCACCCGCGCTGAGTTCTGGCTCTAGCGATGAAGATACAAGATTGAG 3052	QY 2881 GTGCTGAGGTACGATGAGACCCGCACCAGGTGCAGACCCTGCGAGTGTGGCGGTAAACAT 2940	2821 GAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTTTTGACATGACCATGAAGATCTGGAAG	Qy 2761 AGGGGGTGTTCCTACCTTACCAATGCAATTTGAGTCACACTAAGATATTGCTTGAGCCC 2820	OY 2701 GCCTGGCCAGTGTTTGAGCATAACATACTGACCGCTGTTCCTTGCATTTGGGTAACAGG 2760	QY 2641 TGCTCGGACGGCAACTGTCACCTGCTGAAGACCATTCACGTAGCCAGCC	QY 2581 GTGATTAAGCATAACATGGTATGTGGCAACTGCGAGGACAGGGCCTCTCAGATGCTGACC 2640	QY 2521 AGGGTGCGCCACAATGTGGCCTCCGACTGTGGTTGCTTAGTGAAAAAGCGTGGCT 2580	QY 2461 TCAATTAAGAAATGCCTCTTTGAAAGGTGTACCTTGGGTATCCTGTCTGAGGGTAACTCC 2520	QY 2401 CGGGGCTGTGCCTTTTACTGCTGGAAGGGGGTGTGTCGCCCCAAAAGCAGGGCT 2460	QY 2341 GGTGTAAGCTTCTATGGGTTTAACAATACCTGTGTGGAAGCCTGGACCGATGTAAGGGTT 2400	Qy 2281 TTTACTGGCCCCAATTTTAGCGGTACGGTTTTCCTGGCCAATACCAACCTTATCCTACAC 2340	QY 2221 ATGATAAATATGTGGCCGGGGGTGCTTGGCATGGACGGGGTGGTTATTATGAATGTAAGG 2280	2161 TCTGGGAACGGGGCCGAGGTGGAGATAGATACGGAGGATAGGGTGGCCTTTAGATGTAGC	GY 2101 AGGCCAGATTGCAAGTACAAGATCAGCAAACTTGTAAATATCAGGAATTGCTACATT 2160	

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Recombinant viral and non-viral vectors containing the human urokinase plasminogen activator gene and its utilization in the treatment of various types of hepatic, renal, pulmonary, pancreatic and cardiac fibrosis and hypertrophic scars patent: WO 0244393-A 1 06-JUN-2002;

TGT LAB S A DE C V (MX)
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Viruses; dsDNA viruses, no RNA stage;
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GIGHILANGCAINACAIGEIRIG GECANCIGCONGACAGGCCICIC CANAIGE GARCE	TTTTTCCACACCGGGGCGCTGCGGCTGCTGTTGCTTTTTTGAGTTTTATAAAGGATAA 1560	1501 TTTTTCCACACGG	0 \
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TCARTAAGAAATGCCTCTTGAAAGGTGTACCTTGGGTATCCTGTCTGAGGGTAACTCC	AATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTTTGAAATCCTGTGGTGAGCTGTT 1440	1381 AATTAAGGAGGATT             1839 AATTAAGGAGGATT	0 -
CGGGGCTGTGCCTTTTACTGCTGCTGGAAGGGGGTGGTGTGTGCCCCAAAAGCAGGGCT	CAGTACCTCTTGGTTTTGGAGGTTTCTGTGGGGCTCATCCCAGGCAAAGTTAGTCTGCAG 1380	1321 CAGTACCTCTTGGT	0 <
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TTTACTGGCCCOAATTTTAGCGGTACGGTTTTCCTGGCCAATACCAACCTTATCCTACAC	QY GGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCTTGGTTACATCTGACCTCATGGA 1260	1201 GGGGCTTAAAGGGT            1659 GGGGCTTAAAGGGT	0 ~
ATGATAAATATGTGGCCGGGGGTGCTTGGCATGGACGGGTGGTTATTATGAATGTAAGG	QY TGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACTTGCATGGCGTGTTAAATGGGGC 1200	1141 TGATGTAAGTTTAA               1599 TGATGTAAGTTTAA	0 \
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TGCGCTAATGAGCTTGATCTGCTIGCGCGCAGAGTATTCCATAGAGCAGCTGACCACTTAC TGCGCTAATGAGCTTGATCTGCTGGCGCAGAAGTATTCCATAGAGCAGCTGACCACTTAC	TACGGATAGCTGTGACTCCGGTCCTTAACACACCTCCTGAGATACACCCGGTGGTCCC 960	901 TACGGATAGCTGTC	0 ~
TTTAGCTTAATGACCAGACACCGTCCTGAGTGTATTACTTTCAACAGATCAAGGATAAT	CATCACCTGTGTCTAGAGAATGCAATAGTAG 900	841 AATGGCGCCTGCTI	0 ~
AAGGGGTAAAGAAGGAGCGGGGGCTTCTGAGGCTACAAGGGCTAGGAATCTAGCT 19	TGAACCTGAGCCTGAGCCAGAGCCAGAACCGGAGCCTGCAAGACCTACCCGCCGTCCTAA 840	781 TGAACCTGAGCCTC	0 ~
GCIGAACIGIRICCAGAACIGAGACGCATITIGACAATIRCAGAGGATGGCCAGGGCTA	TTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTTTTTAAAAGGTCCTGTGTC 780	721 TTTTACAGTTTTGT             1179 TTTTACAGTTTTGT	0 ~
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Human adenovirus type 5
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
1 (bases 1 to 35935)
Chroboczek, J., Bieber, F. and Jacrot, B.
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Relsdrelmhslqralagtgsgdreaesyfdagadlrwapsrraleaagagpglavap
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Similarity

100.0%;

Score 3052; Pred. No. 0; D; Mismatches

DB 14; 0,

Length 35935;

Indels

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Conservative

<u>,</u>

61 AGAGTTTTCTCCTCCGAGCCGCTCCGACACCGGGACTGAAAATGAGACATATTATCTGCC

120 518 60 0

CGTGTAGTGTATTTATACCCGGTGAGTTCCTCAAGAGGCCACTCTTGAGTGCCAGCGAGT CGTGTAGTGTATTTATACCCGGTGAGTTCCTCAAGAGGCCACTCTTGAGTGCCAGCGAGT

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17774. .17920
VKDSADGYD"
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	1141 TGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACTTGCATGGCGTGTTAAATGGGGC 1200	ag VQ
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1901 1909CIANIONECIIONICCIUS CONTROLINI CONTROLINICATURE CACCACTIAC  [	901 TACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTGAGATACACCCGGTGGTCCC 960	Db 09
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GCTGAACTGTATCCAGAACTGAGACGCATTTTGACAATTACAGAGGATGGGCAGGGGCTA	721 TITTACAGITTTGIGGTTTAAAGAATTTTGTATIGTGATTTTTTAAAAGGTCCTGTGTC 780	용양
1791 GEAGAGECEALIGNARECEGAGACECTEGAGATGAATGATGATGAGGGGCCCCCCGGGACCCTCGGGAATGAAT	661 GAAAATTATGGGCAGTGGTGATAGAGTGGTGGGTTTGGTGTGGTGATTTTTTT	D Qy
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1501 ATGGARGERAARANCECKTEIGHGEGGGGGGGGTACCTGCTGGATITITEIGGCCATGCATCT 102	481 CTGGCTTTCCACCCAGTGACGACGAGGAGTGAAGAGGGTGAGGAGTTTGTGTTAGATTATG 540	유 왕
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1899	361 CCGGTTCTCCGGAGCCGCTCACCTTTCCCGGCAGCCGAGCAGCCGGAGCAGAGAGAG	유 왕
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1321 ANTINA CONCATTA ANA CONCACTA ANA CONTROL AND ANA CONTROL OF THE CONCACTA AND CONCACTA ANA C	241 ATGATTTAGACGTGACGGCCCCCGAAGATCCCCAACGAGGAGGCGGTTTCGCAGATTTTTC 300	B 8
1719 GGCTTCCTTTCGAAGATTTTTCTGCTGTGCGTAACTTGCAGGCAAACAGAGCTCTAA	181 TACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCACCTACCCTTCACGAACTGT 240	B 64
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Unk	ORGANISM	_	2101 AGGCCAGATTGCAAGTACAAGATCAGCAAACTTGTAAATATCAGGAATTGTTGCTACATT 2160
	ACCESSION VERSION KEYWORDS		2041 TGGCTGCAGCCAGGGGATGATTTTGAGGAGGCTATTAGGGTATATGCAAAGGTGGCACTT 2100 
	RESULT 15 AR310582 LOCUS DEFINITION	,	1981 TGCGCTAATGAGCTTGATCTGCTGGCGCAGAAGTATTCCATAGAGCAGCTGACCACTTAC 2040 
459 0	LJ (		1921 TTTAGCTTAATGACCAGACACCGTCCTGAGTGTATTACTTTTCAACAGATCAAGGATAAT 1980 
399 1	Db 3		7 6
941 A	Qy 2		59 GCTGAACTGTATCCAGAACTGAGACGCATTTTGACAATTACAGAGGATGGGCAGGGGCTA 23
339 G	Db 3		801 GCTGAACTGTATCCAGAACTGAGACGCATTTTGACAATTACAGAGGATGGGCAGGGGCTA 186
79	ıω		1741 GCAGAGCCCATGGAACCCGAGAGCCGGCCTGGACCCTCGGGAATGAAT
219 1	рь 3 О <b>у</b> 2		
761 A	Qy 27		681 GATAATACCGACGGAGGAGCAGCAGCAGCAGGAGGAAGCCAAGGCGAGGGGGG
<u> </u>	ω		1621 GTGGAGAGCGGTTGTGAGACACAAGAATCGCCTGCTACTGTTGTCTTCCGTCCG
701	рь 3 Оу 2		
641 T	Qy 2		561 ATGGAGCGAAGAAACCCATCTGAGCGGGGGTACCTGCTGGATTTTCTGGCCATGCATCT 162
039 G	ω		1501 TTTTTCCACACCGGGGCGCGCTGCGGCTGCTGTTGCTTTTTTGAGTTTTTATAAAGGATAA 1560
979 7	Оу 2 2		
521 A	Qy 2		1839 AATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTTTGAAATCCTGTGGTGAGCTGTT 1898 1441 TGATTCTTTGAATCTGGGTCACCAGGCGCTTTTCCAAGAGAAAGGTCATCAAGACTTTTGGA 1500
919 1	Db 2		1 AATTAAGGAGAGTTACAAGTGGGAATTTGAAGAGCTTTTGAAATCCTGTGGTGAGCTGTT 144
859	, h)		1321 CAGTACCTCTTGGTTTTGGAGGTTTCTGTGGGGCTCATCCCAGGCAAAGTTAGTCTGCAG 1380
799 401	Q D D 2		19 GCTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGCGTAACTTGCTGGAACAGAGCTCTAA 17
2341 G  -	Qy 2		261 GGCTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGCGTAACTTGCTGGAACAGAGCTCTAA 132
2739 T	N1		1201 GGGGCTTANAGGGTATATAATGCGCCGTGGGCTAAATCTTGGTTACATCTGACCTCATGGA 1260 
281	Q 5		599 TGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACTTGCATGGCGTGTTAAATGGGGC 165
221 A			1141 TGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACTTGCATGGCGTGTTAAATGGGGC 1200
9	s 83		1539 GCCATAAGGTGTAAACCTGTGATTGCGTGTGTGGGTTAACGCCTTTGTTTG
161 1	Qy 2		479 TATCGAGGACTIGCTIAACGAGCCTGGGCAACCTTIGGACTTGAGCTGTAAACGCCCCCAG 153
559 A	Db 2		.021 TATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACTTGAGCTGTAAACGCCCCAG 108

B 8	₽ 5	, 음 경	g 4	문 &	g Q	B 8	ß 8	B &	B 8	유 성	P &	문 왕	B 8	유 성	Db
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	3458	33 4	333	282 327	3218	3158	C 2640   C 3098	3038	2520	2460	2400	C 2340   C 2798	2280	2220	2618

AR310582 7090 bp DNA
NITION Sequence 18 from patent US 6558948.
SSION AR310582
ION AR310582.1 GI:31703596
DEDS .
CE Unknown.
SANISM Unknown.

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763 TTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCGAGCCAGAACCGGAGCCTGCAAG 8	Oy 583 GGAGGAATACGGGGGACCCAGATATTATGTGTTTCGCTTTTGCTATATGAGGACCTGTGGCA 642	Oy  403 AGCCGGAGGAGAGAGCCTTGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATCG 462	Db 2929 CTACCCTTCACGAACTGTATGATTAGACGTGACGCCCCGAAGATCCCAACGAAGGAGG 2988  Qy 283 CGGTTTCGCAGATTTTTCCCGACCTGTAATGTTGGCGGTGCAGGAAGGA	Oy  103 TGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTGG 162	ORIGIN  ORIGIN  98.5%; Score 3006.8; DB 6; Length 7090;  Best Local Similarity 99.9%; Pred. No. 0;  Matches 3008; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  Matches 3008; TCTTGAGTGCCAGCGAGTAGAGTTTTCTCCTCGGAGCCGCTCCGACACCGGGACTGAAAA 102  Oy  1	Unclassified.  AUTHORS Kochanek, S. and Schiedner, G. AUTHORS Fermanent amniocytic cell line, its production and use for the production of gene transfer vectors  JOURNAL Patent: US 658948-A 18 06-MAY-2003; FEATURES Location/Qualifiers  8 ource /organism="unknown" /mol type="genomic DNA"
Oy  1843 GAGGATGGGCAGGGGCTAAAGGGGGTAAAGAGGGGGGCGCGGGGCTTGTGAGGCTACAGAG	9 GTCTTCCGTCCCCCCGCCATAATACCAGAACCCAAGGAGCAGCAGCAGCAGCAGCAGGAAGCAGC	Db 4189 GGTCATCAAGACTITIGGATTATTTCCACACCCGGGCGCTGCGGGGGGGTACCTGCTTTTTT 4248  Qy 1543 GAGTTTTATAAAGGATAAATGGAGCGAAGAAACCCATCTGAGCGGGGGGTACCTGCTGGA 1602	1363 GGCÀAAGTTAGTCTGCAGAATTAAGGAGATTACAAGTGGGAATTTGAAGAGCTCTTTGAA  1363 GGCÀAAGTTAGTCTGCAGAATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTTTGAA	1183 TGGCGTGTTAAATGGGGGGGGGCTTAAAGGGTATATAATGGGCCGTGGGCTAATCTTGGT	1063 GAGCTGTANACGCCCCAGGCCATAAGGTGTANACCTGTGATTGCGTGTGTGTTAACGCC	Db 3589 TAGAGAATGCAATAGTAGTAGCAGTAGCTGTGACCTCCTAACACACCTCCTGA 3648  Oy 943 GATACACCCGGTGGTCCCCGCTGTAAACCAGTTGCCGTAGAGTTGGTGGGCC 1002

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	3043 ACAGATTGAG 3052            5749 ACAGATTGAG 5758
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2982	2923 GAGTGTGGCGGTAAACATATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGAGCTG
2922	863 ACCATGAAGATCTGGAAGGTGCTGAGGTACGATGAGACCCGCCACCAGGTGCAGACCC
2862	2803 AAGATATTGCTTGAGCCCGAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTTTGACATG
2802	743 TTGCATTTGGGTAACAGGAGGGGGGTGTT 
2742	683 GCCAGCCACTCTCGCAAGGCCTGGCCAG               389 GCCAGCCACTCTCGCAAGGCCTGGCCAG
5388	2623 GCCTCTCAGATGCTGACCTGCTCGGACGGCAACTGTCACCTGCTGAAGACCATTCACGTA
2622 5328	563 CTAGTGAAAAGCGTGGCTGTGATTA 
5268	
5208	443 CGCCCAAAAGCAGGGCT 
2442	383 TGGACCGATGTAAGGGTTCGGGGCTGTG
2382	323 ACCAACCTTATCCTACAC
5028	ACTGGCC
2262 4968	203 GTGGCCTTTAGATGTAGCATGATAAATA?
2202	143 AGGAATTGTTGCTACATTTCT
2142	083 TATGCAAAGGTGGCACTTAGGCCAGAT                 789 TATGCAAAGGTGGCACTTAGGCCAGAT
2082 4788	AGCCAGGGGATGATTI             AGCCAGGGGATGATTI
72	669 CAACAGATCAAGGATAATTGCGCTAATGAGCTTGATCTGCTGGCGCAGAAGTATTCC

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Search completed: October 28, 2005, 06:30:19 Job time : 12695 secs

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04-NOV-2004 (first entry)

ADR41671 standard; DNA; 32802 BP.

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## ALIGNMENTS

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Lytic agent; ds; chaperone; heat shock protein; stimulus; tumour shrinkage; oncolysis; HSP, HSP,-CRA; cancer reactive antigen; nasopharyngeal carcinoma; chondrosarcoma; colon cancer; breast; prostate; ovarian; stomach carcinoma; rectum; malignant hepatoma; melanoma; p53; tumour suppressor gene; variant; genetically modified Ad5; S98-002; E1b region; E3; E1b-55KD; gene; ascites.
                                                                           Hu F,
                                                                                                                     28-JAN-2003; 2003US-0443095P
                                                                                                                                           28-JAN-2004; 2004WO-US002330
                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                              S98-100 (32802bp) adenovirus DNA used as positive control.
                                                      WPI; 2004-580848/56.
                                                                                                                                                                 12-AUG-2004.
                                                                                                                                                                                       WO2004066947-A2.
                                                                                                                                                                                                                                                                             Human adenovirus type 5.
                                                                                                (SHAN-) SHANGHAI SUNWAY BIOTECH CO LTD
                                                                           ₩u B;
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2501. .3328
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Ablating tumor cells in a subject having at least one tumor site contacting the tumor cells in at least one tumor with a lytic age vivo and applying a sufficient in vivo stimulus to the treated tu forming a stimulated tumor.

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The present invention relates to the compositions and methods for ablating tumour cells in a subject having one or more tumour sites. The method includes introduction of a lytic agent into a tumour (which forms a treated tumour) and application of stimulus to the treated tumour. The stimulus (physical, chemical or biological) induces the level of combination of the lytic agent and tumour cells. The stimulus (physical, chemical or biological) induces the level of combination of the lytic agent and tumour cell stimulus leads to tumour shrinkage. The invention relates to the synchronisation between oncolysis and elevated expression of a heat shock protein (HSP), which results in complete or expected the synchronisation between oncolysis of the system in order to elicit an immune response against the cancer. The method of the invention is useful in ablating tumour cells for treating method of the invention is useful in ablating tumour cells for treating maspharyngeal carcinoma, chondrossarcoma, colon cancer, breast cancer, captured oncogene are good candidates for this method of therapy. The concolytic viruses of this invention comprise generically modified Ads cartivated oncogene are good candidates for this method of therapy. The cancer which consist of a defective p53 tumour suppressor gene or an activated oncogene are good candidates for this method of therapy. The concolytic viruses of this invention comprise generically modified Ads variant Ads (899-001) has an extra stop codon at position 2025 (ED) region) and possesses deletions in ED region (in between 27865 and position 30, 95) spe Genetically modified variant passes of the p53 gene and initiates viral replication. The S98-001 variant is not able to the manune system metasic recognition and elimination of E3 is related to which the p53 protein is dysfunctioned. The function of E3 is related to the ability of an adenovirus to escape from the surveillance of the pin genetically modified variant p45. It has deletions in the immune system metasic recognition Query Match Best Local Similarity Example 61 ۲. ATGATTTAGACGTGACGGCCCCCGAAGATCCCCAACGAGGAGGCGGTTTCGCAGATTTTTTC ACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTGGACCAGCTGATCGAAGAGG AGAGTTTTCTCCCTCCGAGCCGCCCCCGACACCCGGGACTGAAAATGAGACATATTATCTGCC 32802 BP; 7543 A; 9233 C; 9139 G; CCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTACTCACTTTTCCGCCGGCGC TACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCACCTACCCTTCACGAACTGT ACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTGGACCAGCTGATCGAAGAGG AGAGTTTTCTCCTCCGAGCCGCTCCGACACCGGGACTGAAAATGAGACATATTATCTGCC CGTGTAGTGTATTTATACCCCGGTGAGTTCCTCAAGAGGCCACTCTTGAGTGCCAGCGAGT CGTGTAGTGTATTTATACCCGGTGAGTTCCTCAAGAGGCCACTCTTGAGTGCCAGCGAGT SEQ Conservative 급 ĕ 100.0%; Score 3052; 100.0%; Pred. No. 0; 3; 129pp; English. ٥, Mismatches DB 13; 6887 T; 0 U; 0 0, Indels Length 32802 0, Gaps 638 180 578 518 698 밁 Ś Ş 밁 á 밁 á á 밁 δ 밁 Ś 밁 밁 Ş 밁 8 밁 Ś 밁 Ś 밁 5 밁 Ş 뫄 밁 Ś 밁 Ś 맑 Ś В Ś 밁 1381 AATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTTTGAAATCCTGTGGTGAGCTGTT 1719 1261 1659 1141 1119 1021 1419 1359 1299 1239 1179 1059 901 841 781 721 601 999 939 879 759 541 481 421 GGCTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGCGTAACTTGCTGCAACAGAGCTCTAA TATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACTTGAGCTGTAAACGCCCCCAG 1080 GCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGCGTCGCCAGGCTGTGGAATG 1020 TACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTGAGATACACCCCGGTGGTCCC CAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGCATGTTTGTCTACAGTAAGT CTGGCTTTCCACCCAGTGACGACGACGAGGATGAAGAGGGTGAGGAGTTTGTGTTAGATTATG CCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCGAGCAGCCGGAGCAGAGAGCCT 420 GGCTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGCGTAACTTGCTGGAACAGAGCTCTAA GGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCTTGGTTACATCTGACCTCATGGA GGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCTTGGTTACATCTGACCTCATGGA 1260 TGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACTTGCATGGCGTGTTAAATGGGGC TGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACTTGCATGGCGTGTTAAATGGGGC 1200 TATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACTTGAGCTGTAAACGCCCCAG TACGGATAGCTGTGACTCCGGTCCTTCTAACACCCTCCTGAGATACACCCCGGTGGTCCC AATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGTCTAGAGAATGCAATAGTAG AATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGTCTAGAGAATGCAATAGTAG TGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAAGACCTACCCGCCGTCCTAA TGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAAGACCTACCCGCCGTCCTAA TTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTTTTTTAAAAGGTCCTGTGTC CAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGCATGTTTGTCTACAGTAAGT TGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCACCGGAGGAGTATACGGGGGACC CTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAGGAGTTTGTGTTAGATTATG CCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCGAGCAGCCGGAGCAGAGAGCCT

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AAC85020 standard; DNA; 33699 ВP

08-MAY-2001 (first entry)

Adenovirus anti-cancer vector GZ1 nucleotide sequence

Adenovirus death protein; ADP; neoplastic; cell death; anti-cancer; gene therapy; cytostatic; GZ1; ds. cancer therapy;

Mastadenovirus

WO200104282-A2

18-JAN-2001

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12-JUL-2000; 2000WO-US018971

12-JUL-1999; 9908-00351778

(UYSL-) UNIV SAINT POUIS

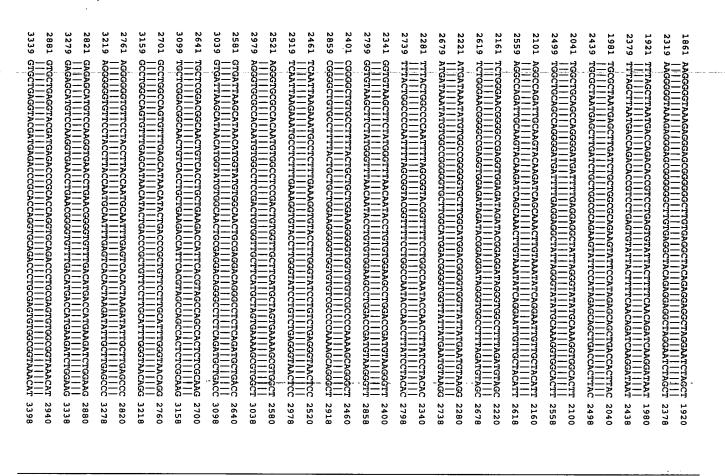
Wold MSM, Toth K, Doronin ζ, Tollefson Æ

WPI; 2001-103079/11.

ARCESULT 2
ARCESOD 2
ARCES Recombinant vector which is replication-competent in a neoplastic cell and overexpresses an adenovirus death protein, useful in cancer therapy when used together with replication-defective adenovirus which expresses an anti-cancer gene.

Claim 5; Page 138-147; 196pp; English

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competent in a neoplastic cell and which overexpresses an adenovirus
death protein (ADP). The vector can be used in a method for promoting
death of a neoplastic cell that comprises contacting the neoplastic cell
with at least one VI; and a composition comprising VI and a second
recombination virus which is: (a) replication defective and which
composition anti-cancer gene product, where VI complements replication
complastic cell: VI, together with one or more replication-defective
adenovirus which expresses an anti-cancer gene product, are useful in
complastic cell: VI, together with one or more replication-defective
adenovirus which expresses an anti-cancer gene product, are useful in
complastic cell: VI, together with one or more replication-defective
adenovirus which expresses an anti-cancer gene product, are useful in
complastic cell: VI, together with one or more replication defective
adenovirus which expresses an anti-cancer gene product, are useful in
complete therapy. Overexpression of ADP by VI results in faster lysis of
complete mucleotide sequence of ADP. The present sequence represents the
complete mucleotide sequence of an adenovirus subgroup C anti-cancer
vector GZI containing E3 deletion and overexpressing ADP
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Best Local
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                                                                                               The invention relates to a recombinant vector (VI) which is replication-competent in a neoplastic cell and which overexpresses an adenovirus death protein (ADP). The vector can be used in a method for promoting death protein (ADP). The vector can be used in a method for promoting death of a neoplastic cell that comprises contacting the neoplastic cell with at least one VI; and a composition comprising VI and a second recombination virus which is: (a) replication defective and which cexpresses an anti-cancer gene product, where VI complements replication of the second recombinant virus; or (b) replication-competent in a composition comprise virus of the second recombinant virus; or (b) replication-competent in a complastic cell. VI, together with one or more replication-defective adenovirus which expresses an anti-cancer gene product, are useful in cancer therapy. Overexpression of ADP VI results in faster lysis of cells and spread of the versus throughout a cell monolayer than viruses expressing wild-type levels of ADP. The present sequence represents the complete nucleotide sequence of an adenovirus subgroup C anti-cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant vector which is replication-competent in a neoplastic cell and overexpresses an adenovirus death protein, useful in cancer therapy when used together with replication-defective adenovirus which expresses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Page 147-156; 196pp; English
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                                                                                                         Adenovirus; pIX; protein IX; gene delivery efficiency; cytostatic; anti-HIV; virucide; gene therapy; geneome;
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30-MAY-2001; 2001US-0293974P
                                       (TRGE ) TRANSGENE SA
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Novel modified adenovirus protein IX and its presence in virus or virus-like particle, useful for improving gene delivery efficiency in target cell of virus or virus-like particle.

Disclosure; Fig 6; 126pp; English.

The invention relates to a novel adenovirus protein IX (pIX) modified by mutation of one or more amino acids of pIX as compared to corresponding wild-type pIX and/or to comprise a binding moiety. The presence of modified pIX in a virus or virus-like particle (VLP) results in improved gene delivery efficiency in the target cell of a virus or VLP as compared to the gene delivery efficiency of a virus or VLP containing wild-type pIX. The protein of the invention has haemostatic, cytostatic, anti-HIV, and virucide activity. The sequence may have a use in gene therapy. The present sequence represents the human adenovirus type 5 genome

Sequence 35934 BP; 8367 A; 10072 C; 9761 G; 7734 T; 0 U; 0 Other;

ş Query Match Best Local Simi Matches 3052; Similarity 100.0%; Score 3052; ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches Mismatches 멂 0, 8 Indels Length 0 0

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1 CGTGTAGTGTATTTATACCCGGTGAGTTCCTCAAGAGGCCACTCTTGAGTGCCAGCGAGT 60	Query Match 100.0%; Score 3052; DB 2; Length 35935; Best Local Similarity 100.0%; Pred. No. 0; Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Sequence 35935 BP; 8367 A; 10074 C; 9760 G; 7734 T; 0 U; 0 Other;	oystrophin gene to the muscle of mice. The EZb-deleted and gutted vectors provide improved adenoviral vectors useful for a wide variety of gene therapy applications. (Updated on 17-OCT-2003 to standardise OS field)	gene products. The invention also provides vectors deleted for all viral coding regions. These 'gutted' vectors permit the transfer of large genes (e.g. up to 35 kb) to cells, as demonstrated by the transfer of the	invention provides improved adenoviral vectors and packaging cell lines. One type of improved vector comprises deletions within the 82b region of the adenoviral genome (see also AAV07261). These E2b-deleted virus are used in conjunction with novel cell lines that constitutively express E2b	Disclosure, Page 69-86; 139pp; English. This nucleotide sequence comprises the adenovirus 5 (Ad5) genome. The	New adeno-viral recombinant plasmid(s) - comprise sequences provided for expression of large foreign DNA fragments, used for, e.g. gene therapy of genetic disease(s).	WPI; 1998-261485/23.	Chamberlain JS, Amalfitano A, Hauser MA, Kumar-Singh R; Hartigan-Occinor DJ;	23-OCT-1996; 96US-00735609. (UNMI) UNIV MICHIGAN.	·· · · · · · · · · · · · · · · · · · ·	30-APR-1998.	Human adenovirus type 5. WO9817783-A1.	Adenovirus 5; Ad5; vector; gene therapy; ds.	Adenovirus 5 genome.	17-OCT-2003 (revised) 28-SEP-1998 (first entry)	AAV07358 ID AAV07258 standard; DNA; 35935 BP. XX AC AAV07258;	NUT 5	TIGGCCTGCACCCGCGCTGAGTTTGGCTCTAGCGATGAAGATACAGATTGAG	CTGGCCTGCACCCGCGCTGAGTTTGGCTCTAGCGATGAAGATACAGATTGAG 3052	2941 ATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGAGCTGAGGCCCGATCACTTGGTG 3000	3339 GTGCTGAGGTACGATGAGACCCGGCACCAGGTGCAGACCCTGCGAGTGTGGCGGTAAACAT 3398	GAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTTTTGACATGACCATGAAGATCTGGAAG	GAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTTTGACATGACCATGAAGATCTGGÀAG 288
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AAC85026 standard; DNA; 35935

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08-MAY-2001 (first entry)

Complete nucleotide sequence of the genome of Ad5.

RESULT 6
AAC85026
ID AAC85
XX AAC8
XX Adenovirus death protein; ADP; neoplastic; cell death; anti-cancer; gene therapy; cytostatic; Ad5; ds. cancer

Mastadenovirus

WO200104282-A2

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The invention relates to a recombinant vector (VI) which is replication-
competent in a neoplastic cell and which overexpresses an adenovirus
death protein (ADP). The vector can be used in an enthod for promoting
death of a neoplastic cell that comprises contacting the neoplastic cell
with at least one VI; and a composition comprising VI and a second
recombination virus which is: (a) replication defective and which
cx expresses an anti-cancer gene product, where VI complements replication
confit the second recombinant virus; or (b) replication-competent in a
neoplastic cell VI, together with one or more replication-defective
adenovirus which expresses an anti-cancer gene product, are useful in
cancer therapy. Overexpression of ADP by VI results in faster lysis of
cells and spread of the virus throughout a cell monolayer than viruses
expressing wild-type levels of ADP. The present sequence represents the
complete nucleotide sequence of the genome of human adenovirus Ad5,
c useful for cancer gene therapy
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Best Local Similarity
Matches 3052; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant vector which is replication-competent in a neoplastic cell and overexpresses an adenovirus death protein, useful in cancer therapy when used together with replication-defective adenovirus which expresses an anti-cancer gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 35935 BP; 8367 A; 10073 C;
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                                                                       ATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGAGCTGAGGCCCGATCACTTGGTG
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ABS69882 standard; DNA; 35935 ₽P

21-NOV-2002 (first entry)

Human adenovirus type 5 genome sequence #1.

RESULT 7
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IID ABS6
XX ABS6
XX ABS6
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XX Vect
XW Vect
XW beta
XW Vect
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XW beta
XW bhen
XW bhen
XW bhen
XW hypo
XW huma
XX H Vector; adenovirus; adeno-associated; adenosine deaminase gene; receptor; adenosine deaminase deficiency; severe combined immune deficiency; PAH; beta-chain; haemoglobin gene; beta-thalassaemia; sickle cell disease; low density lipoprotein gene; familial hypercholesterolaemia; hypoxanthine-guanine phosphoribosyltransferase; Lesch-Nyhan syndrome; phenylalanine hydroxylase gene; gene therapy; phenylketonuria; phenylalanine gene; muscular dystrophy; cystic fibrosis; immunostimulant; human cystic fibrosis transmembrane conductance regulator gene; antinamemic; antilipaemic; nootropic; cytostatic; dermatological; adenovirus genome; ds.

Human adenovirus ņ

US2002102731-A1

01-AUG-2002

12-FEB-2001; 2001US-00782378

02-OCT-2000; 2000US-0237747P

VIND NEW YORK STATE RES FOUND.

۵, Bahou WF, Sandalon Ņ Gnatenko ď

2002-690619/74.

Producing vector, by introducing vector having nucleotide sequence, adenovirus inverted terminal repeats and packaging sequence, and ac associated virus terminal repeat, into cell, and culturing cell. adeno-

Example 2; Page 40-56; 191pp; English

S 밁 ð 밁 Ş 문 S 망 á 밁 á 밁 δ 밁 S 밁 S 8 S 밁 δ 밁 ঠ

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The present invention relates to a new method of producing a vector. method involves introducing recombinant vector having nucleotide sequences. tor. The sequence

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ABS69883 standard; DNA;
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Human adenovirus type 5 genome sequence

hypoxanthine-guanine phosphoribosyltransférase; Lesch-Nyhan syndrome; phenylalanine hydroxylase gene; gene therapy; phenylketonuria phenylalanine hydroxylase gene; gene therapy; phenylketonuria dystrophin gene; muscular dystrophy; cystic fibrosis; immunostimulant; human cystic fibrosis transmembrane conductance regulator gene; antianaemic; antilipaemic; nootropic; cytostatic; dermatological; Vector; adenovirus; adeno-associated; adenosine deaminase gene; receptor; adenosine deaminase deficiency; severe combined immune deficiency; PAH; beta-chain, haemoglobin gene; beta-thalassaemia; sickle cell disease; low density lipoprotein gene; familial hypercholesterolaemia; adenovirus genome; ďs.

Human adenovirus type

US2002102731-A1

12-FEB-2001; 2001US-00782378

02-OCT-2000; 2000US-0237747P

(UYNY ) UNIV NEW YORK STATE RES FOUND.

ָש, Bahou WF, Sandalon 2 Gnatenko

WPI; 2002-690619/74.

Producing vector, by introducing vector having nucleotide sequence, adenovirus inverted terminal repeats and packaging sequence, and ac associated virus terminal repeat, into cell, and culturing cell. adeno-

Disclosure; Page 56-72; 191pp; English

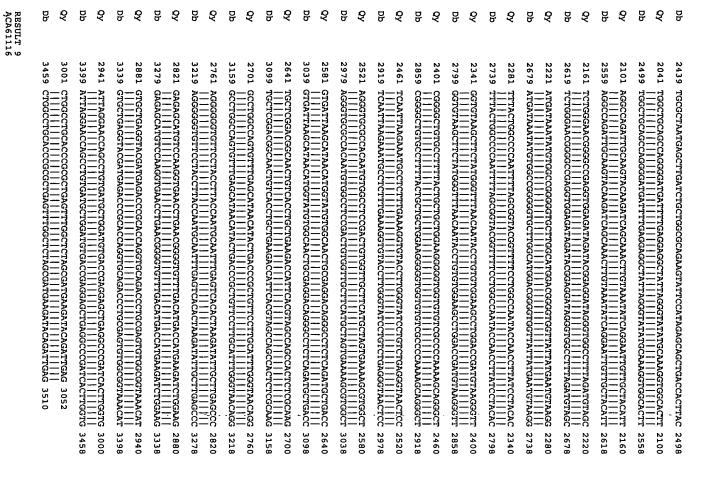
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IID ARBS8883 The present invention relates to a new method of producing a vector. The combined involves introducing recombinant vector having nucleotide sequence (NS) having 5' and 3' end, left and right inverted terminal repeats of compositions are present and adenovirus packaging sequence linked to inverted terminal repeat packaging sequence linked to inverted compositions of the composition of the co

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Best Local Similarity
Matches 3052; Conserv
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                                 AATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGTCTAGAGAATGCAATAGTAG
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                      AATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGTCTAGAGAATGCAATAGTAG
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The invention relates to a nucleic acid encoding a Mét-NS3-NS4A-NS4B-NS5A CC -NS5B (NS stands for non-structural protein from HCV) polypeptide cappearing as ABU09574. The encoded polypeptide has sufficient protease CC activity to process itself to produce an NS5B protein that is enzymatically inactive. Also included are a cultured recombinant cell CC comprising the novel nucleic acid, making an adenovector (comprising: (a) producing an adenovirus genome plasmid comprising a gene expression cC cassette by homologous recombination between the novel nucleic acid and a nucleic acid comprising a first adenovirus region from base pair 1-450 cc corresponding to either Ad5 or Ad6, a second adenovirus region from base pair 3518-5548 corresponding to Ad5 or from base pair 3508-5541 cc corresponding to Ad6, joined to the first region, a third adenovirus region from base pair 3542-28133 corresponding to Ad5 or from base pair 5549-28133 corresponding to Ad5 or from base pair court for adenovirus region from base pair 30789-33784 corresponding to Ad6, joined to the second region, a fourth adenovirus region from base pair 30789-33784 corresponding to Ad6, joined to the third region, and a fifth adenovirus region from base pair 3386-33956 corresponding to Ad5 or from base pair 30789-33784 corresponding to Ad6, joined to the third region, and a fifth adenovirus region from base pair 3385-35759 corresponding to Ad6, joined to the courth region; and (b) rescuing the recombinant adenovirus from the crecombinant adenovirus plasmid), an adenovirus from the crecombinant plasmid), an adenovirus from the first produced by the plasmid and plasmid plasm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding a Met-NS3-NS4A-NS4B-NS5A-NS5B polypeptide, useful as a component of an adenovector or DNA plasmid vaccine for preventing or treating hepatitis C virus.
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13-MAR-2002; 2002US-0363774P.
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adenoviral vector; HCV infection; vaccine; gene therapy;
Sequence 35935 BP;
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adenoviral vector; HCV infection; vaccine; gene therapy; proteas
                                                                                                            Adenovirus serotype 5 genome.
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                      Adenovirus
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13-MAR-2002; 2002US-0363774P
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                                                                                                                                                                                                                    ACA60761 standard; DNA; 35935 BP
                           misc_feature
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/note= "Region of max DNA replication"
63...69
                                  /*tag= b
/rpt_type= OTHER
/note= "OTHER = Inverted terminal repeat (ITR)"
                                                             note= "ETA promoter"
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                                                                           /*tag= a
/standard_name= "Promoter"
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/note= "E4 promoter"
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/bound moiety= '
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/bound_moiety= "ATF"
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Best Local Similarity
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                                                                                                                                                                  The invention relates to a new viral DNA construct encoding for an adenovirus capable of replication in a human or animal tumour cell; that comprises one or more transcription factor (TF) binding sites operatively positioned together with the BIA open reading frame to promote expression of EIA proteins in the presence of the TF. The viral construct and/or virus is useful in the manufacture of a medicament in the therapy of patients having neoplasm, where they are capable of causing death to tumour cell; They are useful in treating malignant and metastatic tumours derived from colon cells particularly liver tumours also for treating colorectal cancers and melanomas. The present sequence represents the DNA sequence of human adenovirus type 5
                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                       New viral DNA construct having one or more tumor specific transcription factor binding sites controlling expression of the EIA open reading frame, useful in the treatment of malignant and metastatic tumors of the
                                                                                                                                                  Sequence 35935 BP; 8367 A; 10073 C; 9761 G; 7734 T; 0 U; 0 Other
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                                                                        ATGATAAATATGTGGCCGGGGGTGCTTGGCATGGACGGGGTGGTTATTATGAATGTAAGG
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CTGGCCTGCACCCGCGCTGAGTTTGGCTCTAGCGATGAAGATACAGATTGAG
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                                                                                                                   GAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTTTGACATGACCATGAAGATCTGGAAG
                                                                                                                                                         AGGGGGGTGTTCCTACCTTACCAATGCAATTTGAGTCACACTAAGATATTGCTTGAGCCC
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Wild type AD5 adenovirus 04-NOV-2004 ADR41672 standard; DNA; 35935 ВP

RESULT 12
ADR41672
ID ADR44
XX ADR4
XX ADR4
XX Wild
XX Util
XX Lyti
XW Lyti
XW Lyti
XW Cum
XW Lytic agent; ds; chaperone; heat shock protein; stimulus; tumour shrinkage; oncolysis; HSP; HSP-CRA; cancer reactive antigen; tumour shrinkage; oncolysis; chondrosarcoma; colon cancer; breast; prost ovarian; stomach carcinoma; rectum; malignant hepatoma; melanoma; p53 tumour suppressor gene; Ad5; S98-002; E1b region; E3; E1b-55KD; gene; misc\_feature Key misc\_feature ascites Human adenovirus /note= "Partial 27865. .30995 Location/Qualifiers 2501. .3328 /\*tag= type ŋ E16 region" prostate;

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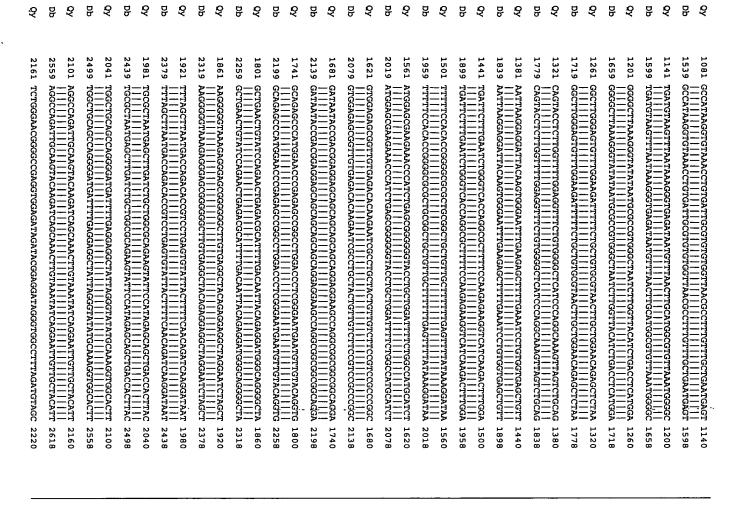
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CC malignant hepatoma, melanoma, ascites etc. Mutations of the p53 gehe CC exist in more than half of cancer cases. The treated or non-treated CC cancers which consist of a defective p53 tumour suppressor gene or an CC activated oncogene are good candidates for this method of therapy. IThe CC oncolytic viruses of this invention comprise genetically modified Ad5 CC variants. This oncolytic adenovirus selectively replicates in cancer CC cells with a p53 mutation and lyses cancer cells with high specificity. CC modified variant Ad5 (598-001) has an extra stop codon at position 2025 CC (EIb region) and possesses deletions in Eib region in specificity. CC modified variant Ad5 (598-001) has an extra stop codon at position 2025 CC (EIb region) and possesses deletions in Eib region (in between 2,501 and CC ells EIb-55KD binds and inactivates the protein encoded by the p53 gene CC replicate in normal cells, but replicates rapidly in cancer cells in CC which the p53 protein is dysfunctional. The function of E3 is related to the ability of an adenovirus to escape from the surveillance of the immune system easier recognition of the E3 region in S98-001 enables CC region encoding E1b-55KD (in between 2,501 and 45. It has deletions in the CC aregion encoding E1b-55KD (in between 2,501 and 3,328) and of the entire CC explicate in cancer cells. So, 598-001 and 399-002 are safe for use in the CC adenovirus DNA. Note: This sequence is the wild type AD5 cc and sequence is the example 1 of the specification. This sequence is referred cc the sequence in example 1 of the specification. This sequence is referred as SEQ ID No 4 in the
Query Match 100.0%; Score 3052; Best Local Similarity 100.0%; Pred. No. 0; Matches 3052; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to the compositions and methods for ablating tumour cells in a subject having one or more tumour sites. The method includes introduction of a lytic agent into a tumour (which|forms a treated tumour) and application of stimulus to the treated tumour. The stimulus (physical, chemical or biological) induces the level of chapperone proteins (heat shock proteins) in the tumour cells. The 'combination of the lytic agent and tumour cell stimulus leads to thmour shrinkage. The invention relates to the synchronisation between onicolysis and elevated expression of a heat shock protein (HSP), which results in sufficient release of HSP-CRA (cancer reactive antigen). The sufficient levels of HSP-CRA exhibit a signal immunogenic enough to the immune system in order to elicit an immune response against the cancer. The method of the invention is useful in ablating tumour cells for treating naconhaverseal carriers chapter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hu F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nasopharyngeal carcinoma, chondrosarcoma, colon cancer, breast cancer, prostate cancer, ovarian cancer, stomach carcinoma, rectum cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ablating tumor cells in a subject having at least one tumor site by contacting the tumor cells in at least one tumor with a lytic agent in vivo and applying a sufficient in vivo stimulus to the treated tumor forming a stimulated tumor.
                                                                            Sequence 35935 BP; 8367 A; 10073 C; 9761 G; 7734 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; SEQ ID NO 4; 129pp; English.
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standard;

16-JUL-2002 (first entry)

Recombinant adenovirus vector GZ3-TERT

RESULT 13
AD27971
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XX Aumar Recombinant adenovirus vector; adenovirus death protein; ADP; telomerase; human; telomerase reverse transcriptase promoter; TERT; neoplastic cell; cancer; GZ3-TERT; E3 region; mutant; ds.

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The invention relates to a recombinant adenovirus vector which is replication-
CC overexpresses an adenovirus death protein (ADP) and which is replication-
CC restricted to cells expressing telomerase, comprises a human telomerase
CC restricted to cells expressing telomerase, comprises a human telomerase
CC reverse transcriptase promoter (hrmn) and at least one inactivating
CC for promoting death of a cell expressing telomerase, and for promoting
CC for promoting death of a cell expressing telomerase, and for promoting
CC death of neoplastic cells in a patient. The adenovirus vector is an
CC efficient and effective anticancer agent that could specifically target
CC neoplastic cells, while replicating poorly or not at all in normal
CC tissue, and efficiently spreading to neighbouring neoplastic cells,
CC thereby maximising its cancer-killing ability. The presence of human
CC telomerase reverse transcriptase promoter allows restriction of
CC coplication of the adenovirus to cells expressing telomerase without the
CC need for complementation to achieve replication competence in these
CC cells. The present sequence is adenovirus vector GZ3-TERT which comprises
CC an ADP gene, a hTERT promoter, and a mutation in the E3 region
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Matches 3052
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Homo sapiens.
Synthetic.
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This invention describes novel permanent amniocyte cell lines (A) containing at least one nucleic acid (I) that causes expression o
                                                                                                               New permanent amniocyte cell lines, useful for producing viral therapy vectors or mutant adenoviruses, express the adenoviral E1B gene products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene therapy; amniocyte; cytostatic; modified tropism; tumor; PCR primer;
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Query Match 98.5
Best Local Similarity 99.9
Matches 3008; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene products (II) of the adenoviral EIA and EIB regions. (A) are used to produce gene therapy vectors, especially adeno, adeno-associated, retro or lenti viral vectors, particularly first- or second generation, large-capacity or deleted adenoviral vectors. (A) are also used to produce adenoviral mutants, optionally with modified tropism. The vectors may express a wide range of therapseutic proteins or antisense RNAs. Adenoviral mutants, unable to express the EIB 55 kDa protein, are useful for treating tumors, they replicate in the cells but not significantly in normal primary cells. (A) can be made efficiently, simply and reproducibly. The products of the invention have cytostatic activity. This sequence represents a PCR primer used in the amplification of adenovirus Ad5 DNA which is described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7090 BP; 1696 A; 1685 C; 1882 G; 1827 T; 0 U; 0 Other;
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                       The specification describes a method of treating cancer or hyperproliferative disorders. The method comprises administering a conditionally replicative viral vector, where at least one of the viral nucleic acids encoding a product essential for its replication is operably linked to an H19 regulatory sequence. The method is useful for treating cancer or hyperproliferative disorders. The cancer is selected from many different types, for example, carcinoma, sarcoma, adenoma and ganglioblastoma. Preferably, the cancer is bladder carcinoma. The present sequence encodes the E1a protein of human adenovirus type 5. It was linked to a H19 regulatory sequence, and used to produce vectors for use in the method of the invention
                                                                                                                                                                                                                      Treating cancer or hyperproliferative disorder comprises administering conditionally replicative viral vector, where the viral nucleic acid encoding a product essential for its replication is operably linked to
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2938	AGGTGCTGAGGTACGATGAGACCCGCACCAGGTGCAGACCCTGCGAGTGTGGCGGTAAAC	2879	Ş
2820	CCGAGAGCATGTCCAAGGTGAACCTGAACCGGGTGTTTGACATGACCATGAAGATCTGGA	2761	뮹
2878	CCGAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTTTTGACATGACCATGAAGATCTGGA	2819	Ş
2760	GGAGGGGGGTGTTCCTTACCAATGCAATTTGAGTCACACTAAGATATTGCTTGAGC	2701	뭥
2818	GGAGGGGGGTGTTCCTACCTTACCAATGCAATTTGAGTCACACTAAGATATTGCTTGAGC	2759	Ś
2700	AGGCCTGGCCAGTGTTTGAGCATAACATACTGACCCGCTGTTCCTTGCATTTGGGTAACA	2641	망
2758	AGGCCTGGCCAGTGTTTGAGCATAACATACTGACCCGCTGTTCCTTGCATTTTGGGTAACA	2699	Ś
2640	CCTGCTCGGACGGCAACTGTCACCTGCTGAAGACCATTCACGTAGCCAGCC	2581	망
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2580	CTGTGATTAAGCATAACATGGTATGTGGCAACTGCGAGGACAGGGCCTCTCAGATGCTGA	2521	B
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ALIGNMENTS

## TITLE JOURNAL COMMENT REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 BM655780 LOCUS ORIGIN FEATURES DEFINITION Query Match Best Local Similarity source 1 (bases 1 to 648) Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L. Celera Anopheles gambiae EST project Unpublished (2002) Seq primer: M13 Reverse Email: HoltRA@celera.com Plate: NU01004A9S row: M Celera Genomics 45 w. Gude Dr., Rockville, Tel: 2404533151 Fax: 2404534580 Anopheles gambiae (African malaria mosquito) Anopheles gambiae Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; BM655780.1 GI:18955291 648 bp mRNA linear EST 26. 17000687386917 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone 19600449669374 5', mRNA sequence. Contact: Holt R.A. BM655780 Anopheles. /clome\_lib="A.Gam.ad.cDNA1" /note="Vector: pSport1; Site\_1: Sal1; Site\_2: Not1; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)." chromosome)" /mol\_type="mRNA" /strain="RSP-ST (Reduced susc. to Permethrin - std. /db\_xref="taxon:7165" /clone="19600449669374" organism="Anopheles gambiae" ocation/Qualifiers dev\_stage="Adult" . .648 lab\_host="DH10b" 20.2%; Score 615.8; DB 4; Pred. No. 5.4e-157; MD 20850, USA column: 20 Length 648; EST 26-FEB-2002

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Unpublished (1997)
Contact: Daniela S. Gerhard, Ph.D.
Coffice of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 766)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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Seq.primer: M13 FORWARD
POLYA-Yes.
                                                    CGGGCACGGTTGCAGGTCTTGTCATTATCACCGGAGGAATACGGGGGGAACCCCAGATATTAT
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/clone lib="Grgan: Lung; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site_1: ECOR I; Site_2: Not I; NCI CGAP FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were cultured in some of the conditions. Control o hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klaph aureus moi 10, 24 hours; Klebsiella moi 10, 3 hours; Staph aureus moi 10, 24 hours; Klebsiella vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; Hadenovirus + LPS 24 hours; Wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours; trand CDNA vector + LPS 3 hours; wt adenovirus + LPS 24 hours; trand CDNA vector + LPS 3 hours; wt adenovirus + LPS 3 hours; hours; hours; hours; wt adenovirus + LPS 3 hours; hours; adenovirus + LPS 3 hours; adenovirus + LPS 24 hours; trand CDNA youtheasis was primed with hot I site.

Gogarage Countries tranded cDNA was ligated to an EcoR I adaptor
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/lab_host="DH10B (Life Technologies)"
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UI-H-FT1-bkb-j-17-0-UI 3', mRNA sequence.
CD370352 CD370352.1 GI:31154442
EST.
                                                                                                                                                                                     Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of
cDNA Library Arrayed by: Dr. M. Bento Soares, University of I
DNA Sequencing by: Dr. M. Bento Soares, University of I
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DNA Sequencing by: Dr. M. Bento Soar
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1 (bases 1 to 750)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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/organism="Homo sapiens"
/mol_type="mRNA"
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                                                                       GTGGTGGGTTTGGTGTGAATTTTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAAT 746
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/clome="UI-H-FTI-bkb-j-17-0-UI"
/tissue_type="Alveolar Macrophage"
/dev stage="Adult"
/lab_host="DH10B (Life Technologies)"
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Ida,H., Boylan,S., Weigel,A., Smit-McBride,Z., Chao,A., Gao,J., Buchoff,P., Wistow,G. and Hjelmeland,L.
Expressed sequence tag analysis of mouse RPE/choroid Unpublished (2004)
Contact: Wistow G
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mil8c08.y1 Mouse RPE/choroid,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAATGTTTAA 1176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGAGAGTTGGTGGGCGTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTAACACACCTCCTGAGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGACATCACCTGTGTCTAGAGAATGCAATAGTAGTAGGGATAGCTGTGACTCCGGTCCTT
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                                                                                                                                                                                                         te: 18 row: c column: 08 primer: M13RP1 reverse primer Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   musculus (house mouse)
                                                                                                                                                                                                                                                                                                            al Eye Institute
NIH, Bethesda, MD 20892-2740,
/tissue_type="RPE/choroid"
/dev stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Mouse RPE/choroid, unamplified: mi/mj"
/note="Organ: Eye; Vector: pSportl; 64ug total RNA
                                                                                                         /db_xref="taxon:10090"
/clone="mil8c08"
                                                                                                                                       /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57Bl6J"
                                                                                          'вех="Male"
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musculus cDNA
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extracted from 200 adult male mouse RPE/choroids. A directionally cloned cDNA library in the pSPORT1 vector(Life Technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter [5'-pGACTAGTCTAGATCGGAGCGGCCGCC(T).5-3']. cDNA was cloned in Not I/Sal I sites. EST analysis was performed the unamplified library at the NIH Intramural Sequencing Center (NISC)."
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ORIGIN

RESULT 5 CA306892/c LOCUS KEYWORDS SOURCE á 밁 S 망 Ś 밁 Ş 밁 Ş 밁 Ś 밁 Ş 밁 8 밁 5 뮹 Ś 밁 ACCESSION 밁 8 VERSION DEFINITION Query Match Best Local ORGANISM Matches 613; 1727 1307 1187 1127 TTTGCTGAATGAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACTTGCATGGC 1667 1607 1547 1487 1427 1367 1247 481 361 301 181 598 541 421 241 121 13 CA306892 743 bp mRNA linear UI-H-FTI-bht-p-24-0-UI.s1 NCI CGAP FTI Homo sapiens UI-H-FTI-bht-p-24-0-UI 3', mRNA sequence. CA306892 GA306892.1 GI:24469946 EST. Homo sapiens (human) Н Homo Similarity CGGCGGCGGCAGGAGCAGAGCCCATGGA 1754 CTGGCCATGCATCTGTGGAGAGCGGTTGTGAGACACAAGAATCGCCTGCTACTGTTGTCT TTTATAAAGGATAAATGGAGCGAAGAAACCCATCTGAGCGGGGGGTACCTGCTGGATTTT GTGTTAAATGGGGCGGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCTTGGTTACA ATCAAGACTTTGGATTTTTCCACACCGGGGCGCCTGCGGCGCTGCTGTTTTTTGAGT TGTGGTGAGCTGTTTGATTCTTTGAATCTGGGTCACCAGGCGCTTTTCCAAGAGAAGGTC AAGTTAGTCTGCAGAATTAAGGAGGATTACAAGTGGGAATTTGAAAGAGCTTTTTGAAATCC GAACAGAGCTCTAACAGTACCTCTTGGTTTTTGGAGGTTTTCTGTGGGGCTCATCCCAGGCA 1366 TCTGACCTCATGGAGGCTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGCGTAACTTGCTG TTTGCTGAATGAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACTTGCATGGC TCCGTCCGCCCGGCAATAATACCGACGGAGG---AGCAACAGCAGGAGGAAGCCAGGCGG TCCGTCCGCCCGGCGATAATACCGACGGAGGAGCAGCAGCAGCAGCAGGAGGAAGCCAGG TTTATAAAGGATAAATGGAGCGAAGAAACCCATCTGAGCGGGGGGTACCTGCTGGATTTT TGTGGTGAGCTGTTTGATTCTTTGAATCTGGGTCACCAGGCGCTTTTTCCAAGAGAAGGTC AAGTTAGTCTGCAGAATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTTTGAAATCC TCTGACCTCATGGAGGCTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGCGTAACTTGCTG GTGTTAAATGGGGGGGGTTAAAAGGGTATATAATGCGCCCGTGGGCTAATCTTGGTTACA sapiens sapiens Conservative 19.4%; 0, Score 592.8; DB 7; Pred. No. 1.1e-150; 0; Mismatches 12; Indels Length cDNA clone EST 05-AUG-2004 ω •• Gaps 1726 540 1666 480 1606 420 1546 360 1486 300 1426 240 180 1306 120 1246 60

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AUTHORS
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Best Local Similarity
Matches 725; Conserv
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Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA: Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtaine
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: M13 FORWARD POLYA=Yes.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from Dr. M. Bento Soares, bento-soares@uiowa.edu
GCAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGAT
                                                                                                                           ACTCACTTTTCCGCCGGCGCCCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCCGA 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified polylinker; Site 1: ECOR I; Site 2: Not I;

NCI_CGAP_FT1 is a normalized cDNA library_constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; CPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; Klebsiella
moi 10, 3 hours; Klebsiella moi 10, 24 hours; Klebsiella
moi 10, 3 hours; Staph aureus moi 10, 24 hours; Klebsiella
moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector
(Ad5 CMV eGFP), moi 500, 24 hours; Wt adenovirus moi 500,
3 hours; Wt adenovirus moi 500, 24 hours; Adenovirus + LPS
3 hours; Ad vector + LPS 24 hours; Wt adenovirus + LPS 3
hours; Wt adenovirus + LPS 24 hours. The library was
normalized according to Bonaldo, Lennon and Soares, Genome
Research, 6:791-806, 1996. First strand cDNA synthesis was
primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EGGR I adaptor,
digented with Not I and cloned directionally into
                                                                                                                                                                                                                                                                                                                                                                      digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
                                                                                                                                                                                                                                                                                                                       TAG_LIB=UI-H-FT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="NCI_CGAP_FT1"
/note="organ: Lung; Vector: pT7T3-Pac_(Pharmacia) with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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|tissue_type="Alveolar Macrophage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
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lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                              19.2%;
86.0%;
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                                                                                                                                                                            0,
                                                                                                                                                                          Score 587.4; DB
Pred. No. 3.4e-14
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                 Alveolar Macrophage
                                                                                                                                                                                              1; DB 6;
3.4e-149;
                                                                                                                                                                          Indels 117;
                                                                                                                                                                                                                        Length 743;
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                            460
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                                                                        REFERENCE
AUTHORS
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                         Tumor Gene Index
Unpublished (1997)
                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 726)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Homo sapiens
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cDNA clone

1179

80 1120 140 1060 200 1000

260 940 320 880 380

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FEATURES
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nes 710; Conser
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Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@miiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-21, par rich#wow_complexity (matched compliment)
                                                                                                        CTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGACGATGAAGAGGGTGAGGAGTTTTGT
                                                                                                                                                                                                                                                                             TCCGCCGGCGCCCGGTTCTCCGGAGCCGCCTCACCTTTCCCCGGCAGCCCGAGCCCGGA 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /(alone lib="World (Lale recumologies)"
//clone lib="Worl CGAP FT1"
//note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP FT1"
NCI CGAP FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; LPS 100 ng/ml, 24 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; klabsiella moi 10, 3 hours; Klabsiella moi 10, 4 hours; Klabsiella moi 10, 3 hours; Staph aureus moi 10, 24 hours; Klabsiella vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; Hadenoviral vector the S 24 hours; wt adenoviral vector the S 24 hours; wt adenoviral vector the S 24 hours; wt adenoviral vector the S 25 hours; hadenoviral to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site.

Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT) la tail. The sequence tag for this library is GCCATGCCG. The tissue was provided by Dr. Gary W.

The TTSUETE-Hyman Lung Alveolar Macrophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAG_TIŠSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"
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UI-H-FT1-bjz-n-11-0-UI.s1 NCI CGAP FT1 Homo sapiens cDNA clone
UI-H-FT1-bjz-n-11-0-UI 3', mRNA sequence.
CD370856 CD370856.1 GI:31154946
                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
                                                 http://genome.uiowa.edu/distribution/cgap.html
                                                                                                                                                                                                                                                                          Unpublished (1997)
                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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Seq primer: M13 FORWARD
POLYA=Yes.
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                                                                           cDNA Library preparation: Dr. M. Bento Soares, University of CDNA Library Arrayed by: Dr. M. Bento Soares, University of DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at
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                                               TGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCCGGAGCCTGCAAGACCTACCCGCCG 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCACCCGGAGGAATACGG 594
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                                                                                                                                                                                                                                                                                                                                                                             GGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGCATGTTTGTCTACA 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCACCGGAGGAATACGG 483
                                                                                                                                                                                                                          //clone lib="World CARP F71"
//clone lib="Worl Carp F753-Pac (Pharmacia) with a modified polylinker; Site 2: Not I;
//clone lib="Worl Carp F753-Pac (Pharmacia) with a modified polyline from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations of the redonor macrophages in different
conditions, other donor m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .602
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAG_TISSUE=Human Lung Alveolar Macrophage TAG_LIB=UI-H-FT1
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/tissue_type="Alveolar Macrophage"
/dev stage="Adult"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ=GGCCATGCCG"
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83.5%;
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Query Match 11.0%;
Best Local Similarity 99.7%;
Matches 336; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: HoltRA@celera.com Plate: NU01004AB8 row: |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Celera Genomics
45 w. Gude Dr., Rockville,
Tel: 2404533151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (Dases 1 to 337)
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L. Celera Anopheles gambiae EST project
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BM591710.1 GI:18887571
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17000687388831 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA clone
19600449695952 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: 2404534580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anopheles.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACTTGAGCTGTAAACG 107-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGGCGTCGCCAGGCTGT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGCGTCGCCAGGCTGT 1014
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                                                                                                                                                                                                                                                                                                                                                                                                                                    primer: M13 Reverse
                                                                                                /clone lib="A.Gam.ad.cDNA.blood1"
/note="Vector: pSport1; Site 1: Sal1; Site 2: Not1; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen 24 hours after human blood feeding. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)"
                                                                                                                                                                                                                                                                                                                 chromosome) "
                                                                                                                                                                                                                                                                                                                                 /organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc
                                                                                                                                                                                                                                       /dev_stage="Adult"
/lab_host="DH10b"
                                                                                                                                                                                                                                                                            clone="19600449695952"
                                                                                                                                                                                                                                                                                                db_xref="taxon:7165"
                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
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  Score 335.4; DB 4
Pred. No. 3.4e-80;
0; Mismatches 1
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                                      Length 337;
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
BF915148
                                                                                                                                                                                 Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-UT0114-
041200-328-H03_1&t3=2000-12-04&t4=1)
Seq_primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shotgun sequencing
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1 (bases 1 to 347)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BF915148
                                                                                                                                                                                                                                                                                          Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTTGCTGAATGAGTTGAAGTTTAATAAAGGGTGAGATAATGTTTAACTTGCATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAGTTAGTCTGCAGAATTAAGGAGGATTACAAGTGGGAATTTTGAAGAGCTTTTTGAAATC
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                                                                                                                                                                       quality
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/clone lib="UT0;14"
/note="Organ: uterus tumor; Vector: puc18; Site_1: Smal;
/note="Organ: h mini-library was made by cloning product:
                                                                                                                                                   ity sequence stop: 329.
Location/Qualifiers
                                                                 /mol_type="mRNA"
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/dev_stage="Adult"
                                                                                                                   organism="Homo sapiens"
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                                                 lib="UT0114"
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                                                                                                                                                                                                                          Brazil
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                 /organism="Homo sapiens"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 323)

Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                        Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-UT0114-
011200-362-G09_1&t3=2000-12-01&t4=1)
Seq primer: puc 18 forward
122
                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
                                                                                                                                                                                                             Fax: +55-11-2707001
                                                                                                                                                                                                                                      Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF
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IL3-UT0114-011200-362-G09_1 UT0114
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milarity 95.5%;
Conservative (
quality sequence stop:
Location/Qualifiers
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Pred. No. 1e-56;
O; Mismatches
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/mol\_type="mRNA" /db\_xref="taxon:9606"

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JOURNAL
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AUTHORS
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BF915126/c
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                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 321)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                             Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtm12.pl?tl=IL3&t2=IL3-UT0114-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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IL3-UT0114-041200-328-A10_1 UT0114
                                                               Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                       sequence tags
Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                        +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens
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/clone_lib="UT0114"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:12306584
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Pred. No. 1.1e-49;
0; Mismatches 13;
                                                                                                                                                                                                                                                                           97
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SOURCE
ORGANISM
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VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
CD366021/c
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Matches 2
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                                                                      Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/cgap.html
                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 741) NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Mational Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                               CD366021 741 bp mRNA linear UI-H-FT1-bjs-k-22-0-UI.81 NCI CGAP FT1 Homo sapiens UI-H-FT1-bjs-k-22-0-UI 3', mRNA sequence. CD366021 CD366021.1 GI:31150111 EST.
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                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
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Seg primer: puc 18 forward
High quality sequence stop: 159.
                                                                                                                                                                                                                                           Unpublished (1997)
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                                                         primer: M13 FORWARD
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Location/Qualifiers
1. .741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
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95.1%;
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Pred. No. 1.4e-49;
0; Mismatches 12;
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ACCESSION
VERSION
                                                                                                                                                                                                                            RESULT 13
CD742922/c
                                                                                                                                   DEFINITION
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234;
                                                                               CD742922
667 bp mRNA linear EST 05-AUG-UI-H-FT1-bka-k-23-0-UI.sl NCI CGAP_FT1 Homo sapiens cDNA clone UI-H-FT1-bka-k-23-0-UI 3', mRNA sequence.
    CD742922
CD742922.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of
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/lab_host="DH10B (Life Technologies)"
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/tissue_type="Alveolar Macrophage"
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98.7%;
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                                                                                                                                                                                  EST 05-AUG-2004
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Query Match 5. Best Local Similarity 97.8 Matches 176; Conservative

5.7%;

Score 173.6; DB 6; Pred. No. 9.7e-36; 0; Mismatches 4;

Length 667;

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Tissue Procurement: Dr. Gary M. Hunninghake, U of I

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
Clone Distribution, edu/distribution/cgap.html
The following repetitive elements were found in this cDNA
sequence: 546-595, v.(CAG)n#Simple_repeat (matched compliment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: M13 FORWARD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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1 (bases 1 to 667)
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                                                                                                                                          /clone lib="World Charge From the Chinology easy."
/clone = Torgan: Lung; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP From 1s a normalized cDMA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; control 10 ng/ml, 24 hours; control 24 hours; LPS 100 ng/ml, 24 hours; control 24 hours; LPS 100 ng/ml, 24 hours; Staph aureus moi 10, 3 hours; Klebsiella moi 10, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Klebsiella vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenovirus + LPS 3 hours; Adenovirus + 
                               TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"
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/lab_host="DH10B (Life Technologies)"
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/db_xref="taxon:9606"
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|mol_type="mRNA"
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CD365243/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs remail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

CDNA Library preparation: Dr. M. Bento Soares, University of

CDNA Library Arrayed by: Dr. M. Bento Soares, University of

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found a

http://genome.uiowa.edu/distribution/cgap.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CD365243 661 bp mRNA 1
UI-H-FT2-bjj-c-23-0-UI.81 NCI CGAP FT2 Homo
UI-H-FT2-bjj-c-23-0-UI 3', mRNA sequence.
CD365243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
1 (bases 1 to 661)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens
/clone lib="MCI CGAP PT2"

/notes "Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR ; Site 2: Not 1; NCI CGAP PT2 is a subtracted cDNA library-constructed from a pool of 81 RNA samples from Alveolar Macrophages; challenged with different treatments. The mRNA samples challenged with different treatments the mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; hours; LPS 100 ng/ml, 24 hours; Rebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Wadenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Wadenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Wadenoviral vector + LPS 3 hours; Wadenovirus + LPS 3 hours; Wadenovirus + LPS 3 hours; Wadenovirus + LPS 24 hours; Wadenovirus + LPS 3 hours; Wadenovirus + LPS 24 hours; Wadenovirus + LPS 3 hours; Wadenovirus + LPS 24 hours; Wadenovirus + LPS 3 hours; Wadenovirus + LPS 3 hours; Wadenovirus + LPS 24 hours; Wadenovirus + LPS 3 hours; Wadenovirus + LPS 3 hours; Wadenovirus + LPS 24 hours; Wadenovirus + LPS 3 hours; Wadenovirus + LPS 3 hours; Wadenovirus + LPS 3 hours; Wadenovirus + LPS 24 
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/clone="UI-H-FT2-bjj-c-23-0-UI"
/tlssue_type="Alveolar Macrophage"
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'lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
|mol_type="mRNA"
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Matches 173;
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FEATURES

COMMENT

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2886 GAGGTACGATGAGACCCGCACCAGGTGCAGACCCTGCGAGTGTGGCGGTAAACATATTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             661 GAGGTACGATGAGACCCGCACCAGGTGCAGACCCTGCGAGTGTGGCGGTAAACATATTAG
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167; Conserv
                                                                                                                                                                                                                                                                                                                                                          Email: HoltRA@celera.com
Plate: NU01004AAI row: J
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BM600614 173 bp n
17000687054399 A.Gam.ad.cDNA.blood1
19600449720751 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 w. Gude Dr., Rockville, Tel: 2404533151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Celera Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Holt R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Celera Anopheles gambiae EST project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Holt, R.A., Lin, J.-J., Murj
Charlab, R., Collins, F.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neoptera; Endopterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anopheles gambiae
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                                                                                                                                                                                                                                                                                                                                                                                                                             2404534580
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/clone lib="A.Gam.ad.cDNA.blood1"
/note="Vector: pSport1; Site 1: Sal1; Site 2: Not1; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen 24 hours after human blood feeding. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of Iowa.
TAG_TISSUE=Human Lung
TAG_LIB=UI-H-FT2
                                                                                                                                                                                                                                chromosome) "
                                                                                                                                                 /clone="19600449720751"
/dev_stage="Adult"
/lab_host="DH10b"
                                                                                                                                                                                                                                                    /organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAG_SEQ=GGCCATGCCG"
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                                                                                                                                                                                                                 db_xref="taxon:7165"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 167;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diptera;
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| Anopheles
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es gambiae cI
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Conservative

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Indels

1;

Gaps

Score 162; DB 4 Pred. No. 1e-32; 0; Mismatches

DB 4;

Length 173;

5.3%;

Search completed: October 28, 2005, 08:56:38	Search o
121 ATCTGACCTCATGGAGGCTTGGGAGTGTTTGGAAGA-TTTTCTGCTGTGCGTAA 173	Db
1246 ATCTGACCTCATGGAGGCTTGGGAGGTGTTTGGAAGATTTTTCTGCTGTGCGTAA 1299	Q
61 CGTGTTAAATGGGGCGGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCTTGGTTAC 120	9
1186 CGTGTTAAATGGGGCGGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCTTGGTTAC 1245	Ş
1 GTTTGCTGAATGAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACTTGCATGG 60	Вb
1126 GTTTGCTGAATGAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACTTGCATGG 1185	δ

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Result
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Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-09-244-752-1
US-09-245-497-1
US-09-562-919-1
US-09-956-335-2
US-08-735-609-4
US-08-735-609-4
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TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic ac:
DESCRIPTION: /desc = "DNA"
US-08-735-609-1
           ફ
                                                                              Query Match 100.0%; 18est Local Similarity 100.0%; 19est Local Similarity 00.0%; 19est Local Similarity 00.00%; 10est Local Similarity 10
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US-08-735-609-1 US-08-735-609-1 Sequence 1, Application US/08735609 Patent No. 5955360 Patent No. 1000 Andrea Paplicant: Hauser, Michael A. Paplicant: Hauser, Michael A. Paplicant: Hardigan-O'Connor, Dennis J. Paplicant: Southers: 1000 Additional States of America Paplicant: Landigan States Of American Paplicant Landigan States Of Americ	00 2 US-08-473-399B-3 Sequence 00 3 US-08-853-831-1 Sequence 00 4 US-09-510-885-1 Sequence 00 4 US-09-510-885-3 Sequence 00 5 PCT-US93-09774-1 Sequence 00 5 PCT-US93-09774-3 Sequence 00 5 PCT-US93-09774-3 Sequence 01 5 US-08-923-137-1 Sequence 02 4 3 US-08-923-137-1 Sequence 03 4 US-09-713-678-39 Sequence 04 US-08-752-760A-1 Sequence 05 4 US-08-653-114A-1 Sequence 07 4 US-08-653-114A-1 Sequence 08 US-08-540-077-4 Sequence 09 US-08-540-077-2 Sequence 15 3 US-08-945-424-1 Sequence 15 3 US-08-945-424-1 Sequence 15 4 US-09-718-865-1 Sequence	8 1000 32.8 1000 2 US-08-473-399B-1 Sequence

Score 3052; Pred. No. 0; 0; Mismatches

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DB 0, 2 acid

241 ATGATTIAGACGTGACCGCCCCCACAAATCCCCACCAACAGCCGTTTTCCCAAATTTTTC 300 639 ATGATTIAGACGTGACCGCCCCCAAAATCCCAAACGGATTTCCCCAAATTTTTC 758 301 CCCGACTCTGTAATGTTGCCGGTCACGAAAGGAATTGCCTAACGGGTTTTCCGCCGCGCGCG	
1779 CAGTACCTCTTGGTTTTGAGAGGTTCTGCGGGCTCTGCCAGGCAAAGTTGGAAATCCCAGGGAAATTCTGCAAATTCGAAATTCGAAATTCGAGAGATTTGAAAGAGCTTTTTGAAATTCCCAGGGCAAATTCGACGTTTTTGAAATTCCTGTTTTTGAAATTCCTGTTTTTGAAATTCCTGTTTTTGAAATTCCTGTTTTTGAAATTCCTGTTTTTTTT	Db 1539 GCCATAAGGTGTAAACCTGTGATTGCTGTGTTTAACCTTTGCTTTGCTTGAATGAGT 1598  Qy 1141 TGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACTTTGCATGGGCGTGTTAAATGGGC 1200

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RESULT 2
US-08-735-609-1
Sequence 1, Application Us
Patent No. 5994132
Patent INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chambe
APPLICANT: Thambe
APPLICANT: Chamberlain, Jeffrey S.
Amalfitano, Andrea
Hauser, Michael A.
Kumar-Singh, Rajendra
Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEB: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
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FILING DATE: 23-Oct-1996
CLASSIFICATION: <-Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 3052; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOPTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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STATE: California
COUNTRY: United States
                                                                                   CTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAGGAGTTTGTGTTAGATTATG
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521 979	S B 8	441 TGATTCTTTGAATCTGGGTCACCAGGCGCTTTTCCAAGAGAGAG
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9 1	p Q	321 CAGTACCTCTTGGTTTTTGGAGGTTTCTGTGGGGCTCATCCCAGGCAAAGTTAGTCTGCAG 13 
2341 GGTGTAAGCTTCTATGGGTTTAACAATACCTGTGTGGAAGCCTGGACCGATGTAAGGGTT	Db	261 GGCTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGCGTAACTTGCTGGAACAGAGCTCTAA 
2281 TTTACTGGCCCCAATTTTAGCGGTACGGTTTTCCTGGCCAATACCAACCTTATCCTACAC	D Q	01 GGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCTTGGTTACATCTGACCTCATGGA 12 
9 1	g Qq	141 TGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACTTGCATGGCGTGTTAAATGGGGC 12 
2161 TCTGGGAACGGGCCGAGGTGGAGATAGATACGGAGGATAGGGTGGCCTTTAGATGTAGC	₽ <b>Q</b>	081 GCCATAAGGTGTAAACCTGTGATTGCGTGTGTGGTTAACGCCTTTGTTTG
2101 AGGCCAGATTGCAAGTACAAGATCAGCAAACTTGTAAATATCAGGAATTGTTGCTACATT	р <i>Q</i>	021 TATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACTTGAGCTGTAAACGCCCCAG 108
41 99	D Q	961 GCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGCGTCGCCAGGCTGTGGAATG 1020 
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	B &	661 GAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTGTGGTAATTTTTT
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OY 1 CGTGTAGTGTATTTATACCCGGTGAGTTCCTCAAGAGGCCACTCTTGAGTGCCAGCGAGT 60	Query Match  100.0%; Score 3052; DB 3; Length 35935;  Best Local Similarity 100.0%; Pred. No. 0;  Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	∾¤ O 🖺	4- 0	ATTORNEY/AGENT INFORMATION:  NAME: Dadio, Susan M.  REGISTRATION NUMBER: 40,373  REFERENCE/DOCKET NUMBER: 029395-002		FILING DATE: 26-7007379732 FILING DATE: 26-70AN-1995 CLASSIFICATION: 435 FRIOR APPLICATION DATA: APPLICATION NIMBER: WO DCT/FR94/00624	ARG	ZIP: 22314-2756 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible	et, Suite 500	VENTION: COMPLEMENTATION LINES SEQUENCES: 43 NCE ADDRESS: DOANG SWEGVER S MARHIS I	NI,	US-08-379-452-43; Sequence 43, Application US/08379452; Patent No. 6040174	3459	OP 3001 CTGGCCTGCACCCGCGCTGAGGTTTGGCTCTAGCGATGAAGATACAGATTGAG 3052	2941 ATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGAGCTGAGGCCCGATCACTTGGTG	OY 2881 GTGCTGAGGTACGATGAGACCCGCACCAGGTGCAGACCCTGCGAGTGTGGGGGTAAACAT 2940	QY 2821 GAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTTTGACATGACCATGAAGATCTGGAAG 2880	QY 2761 AGGGGGTGTTCCTACCTTACCAATGCAATTTGAGTCACACTAAGATATTGCTTGAGCCC 2820
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1539 GCCATAAGGTGTAAACCTGTGATTGCGTGTGGTTAACGCCTTTGTTTG	TATCGARGACTTGCTTAACGARCCTGGCCAACCTTTGGACTTTAACGCCCCAG 10	961 GCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGCGTCGCCAGGCTGTGGAATG 1020	901 TACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTGAGATACACCCGGTGGTCCC 960 	841 AATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGTCTAGAGAATGCAATAGTAG 900 	781 TGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAAGACCTACCCGGCGGTCCTAA 840	721 TTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTTTTTTAAAAGGTCCTGTGTC 780 	661 GAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTGTGGTAATTTTTT	601 CAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGCATGTTTGTCTACAGTAAGT 660 	541 TGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCACCGGAGGAATACGGGGGGACC 600	481 CTGGCTTTCCACCCAGTGACGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	421 TGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATCGATC	361 CCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCGAGCAGAGCAGAGAGAG	301 CCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTACTCACTTTTCCGCCGGCGC 360	241 ATGATTTAGACGTGACGGCCCCGAAGATCCCAACGAGGAGGCGGTTTCGCAGATTTTTC 300	TACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCACCTACCCTTCACGAACTGT	579 AddaAgdrdThATTACCGAAGAAATGGCCGCCAGTCTTTGGACCAGCTGATCGAAGAGG 638 181 TACTGGCTGATATCTTCCACCTTCCTAGCCATTTTGAACCACCTTACCCTTACGAACTGT 240	519 AGAGTTTTCTCCTCCGAGCCCGCTCCGACACCGGGACTGAAAATGAGACATATTATCTGCC 578  121 ACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTGGACCAGCTGATCGAAGAGAG 180	459 CGTGTAGTGTATTTATACCCCGGTGAGTTCCTCAAGAGGCCACTCTTGAGTGCCAGCGAGT 518 61 AGAGTTTTCTCCTCCGAGCCGCTCCGACACCCGGGACTGAAAATGAGACATATTATCTGCC 120

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	CCAGATTGCAAGTACAAGATCAGCAAACTTGTAAATATCAGGAATTGTTGCTAGGAACGGAGGAGAGTGGCCTTTAGATCGGAAGGAGAGGGGCCGAGGTGGAGATAGAT
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	1981 TGCGCTAATGAGCTTGATCTGCTGGCGCAGAAGTATTCCATAGAGCAGCTGACCACTTAC 2040 
Db 43	1921 TTTAGCTTAATGACCAGACACCGTCCTGAGTGTATTACTTTTCAACAGATCAAGGATAAT 1980 
S B &	1861 AAGGGGGTAAAGAGGGAGCGGGGGGGCTTGTGAGGCTACAGAGGAGGCTAGGAATCTAGCT 1920 
מם א	1801 GCTGAACTGTATCCAGAACTGAGACGCATTTTGACAATTACAGAGGATGGGCAGGGGCTA 1860 
S B 4	1741 GCAGAGCCCATGGAACCCGAGAGCCGGCCTGGACCCTCGGGAATGAAT
δ β <del>γ</del>	1681 GATAATACCGACGAGGAGCAGCAGCAGCAGGAGGAAGCCAGGCGGC
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S B 7	1321 CAGTACCTCTTGGTTTTGGAGGTTTCTGTGGGGCTCATCCCAGGCAAAGTTAGTCTGCAG 1380 
\$ B #	1261 GGCTIGGGAGIGTTIGGAAGAITTTICTGCTGTGCGTAACTIGCTGGAACAGAGCTCTAA 1320 
S B 8	1201 GGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCTTGGTTACATCTGACCTCATGGA 1260 
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Sequence 1, Application US/09315372
Sequence 1, Application US/09315372
Sequence 1, Application US/09315372
Sequence 1, Application US/09315372
Sequence 1, Application, Jeffrey S.
APPLICANT: Chamberlain, Jeffrey S.
APPLICANT: Hauser, Michael A.
APPLICANT: Kumar-Singh, Rajendra
APPLICANT: Hartigan-O'Connor, Dennis J.
APPLICANT Hartigan-O'Connor, Dennis J.
APPLICANT HARTON: IMPROVED ADENOVIRUS VECTORS
NUMBER OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
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1 TGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCACCGGAGGAATACGGGGGACC	481 CTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGTGAGGAGTTTGTGTTAGATTATG		Oy 361 CCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCGAGCAGCCGAGCAGAGAGAG	QY 301 CGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTACTCACTTTTCCGCCGGCGC 360	241 ATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGGAGGCGGTTTCGCAGATTTTTC	QY 181 TACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCACCTACCCTTCACGAACTGT 240	121 ACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTGGACCAGCTGATCGAAGAGG	Qy 61 AGAGTTTTCTCCTCCGAGCCGCTCCGACACCGGGACTGAAAATGAGACATATTATCTGCC 120	CGGTGAGTTCCTCAAGAGGCCACTCTTGAGTGCCAC	uer est atc	~ o B	SEQUENCE CHARACTERISTICS: LENGTH: 35935 base pairs TYPE: nuclei acid STPANDENNESS: double		ATTORNEY/AGENT INFORMATION:  NAME: Ingolia, Diane E.  REGISTRATION NUMBER: 40,027  REFERENCE/DOCKET NUMBER: 1M4-102484	CLASSIFICATION: PRIOR APPLICATION DATA: PRIOR APPLICATION NUMBER: US 08/735,609 PILING DATE:	SOFTWARE:   Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/315,372 FILING DATE:	COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk  COMPUTER: IIM PC compatible  OPERATING: SYSTEM: PC-DOS/MS-DOS	STATE: California COUNTRY: United States Of America ZIP: 94104
Oy 1621 GTG	Qy 1561 ATC     Db 2019 ATC	Oy 1501 TT7       Db 1959 TT7	9 1	1381	1321 1779	Qy 1261 GGC     Db 1719 GGC	Qy 1201 GGC     Db 1659 GGC	Qy 1141 TGF     Db 1599 TGF	Qy 1081 GCC     Db 1539 GCC	1021 1479	Qy 961 GCT     Db 1419 GCT	Qy 901 TAC     Db 1359 TAC	Qy 841 AA7     Db 1299 AA7	Qy 781 TGF     Db 1239 TGF	Qy 721 TTT     Db 1179 TTT	Qy 661 GAJ     Db 1119 GAJ	Qy 601 CAC     Db 1059 CAC	Db . 999 TGC
GTGGAGAGCGGTTGTGAGACACAAGAATCGCCTGCTACTGTTGTCTTCCGTCCG	ATGGAGCGAAGAAACCCATCTGAGCGGGGGGTACCTGCTGGATTTTCTGGCCATGCATCT 1620	TTTTTCCACACCGGGGGGGGCTGCGGCTGCTGTTGCTTTTTTGAGTTTTATAAAGGATAA 1560				GGCTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGGGTAACTTGCTGGAACAGAGCTCTAA 1320	GGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCTTGGTTACATCTGACCTCATGGA 1260	TGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACTTGCATGGCGTGTTAAATGGGGC 1200 			GCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGCGTCGCCAGGCTGTGGAATG 1020	TACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTGAGATACACCCCGGTGGTCCC 960	AATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGTCTAGAGAATGCAATAGTAG 900	TGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAAGACCTACCCGCCGTCCTAA 840	TITIACAGITITGIGGITIAAAGAAITTIGIATTGIGATTITITTAAAAGGICCTGIGIC 780	GAAAATTATGGGCAGIGGGIGATAGAGTGGTGGGTTTGGTGTGGTAATTTTTTTT	CAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGCATGTTTGTCTACAGTAAGT 660	

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RESULT 5
US-09-244-752-1
                                                                         US-09-244-752-1
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APPLICANT: Hauser, Michael A.
APPLICANT: Hauser, Michael A.
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VEC
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
STATE: California
                                                                                                                               TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09244752
Patent No. 6063622
GENERAL INFORMATION:
APPLICANT: Chamberlain, Jeffrey
APPLICANT: Amalfitano, Andrea
Query Match
Best Local Similarity
Matches 3052; Conserv
                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,752
                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                 MOLECULE TYPE:
                                                                                             DESCRIPTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: UI
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Sequence 1, Application US/09245497

Patent No. 6083750

GENERAL INFORMATION:

APPLICANT: Chamberlain, Jeffrey S.

APPLICANT: Amalficano, Andrea

APPLICANT: Hauser, Michael A.

APPLICANT: Kumar-Singh, Rajendra

APPLICANT: Hartigan-O'Connor, Dennis J.

APPLICANT: Hartigan-O'Connor, Dennis J.

TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:
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TYPE: nucleic acid
STRANDEDESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic
DESCRIPTION: /desc = "DNA"
US-09-245-497-1
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APPLICATION NUMBER: «B) FILING DATE:
APPLICATION NUMBER: «B) FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: INGOlia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 1:
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Best Local Similarity
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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STREET: 220 Montgomery Street, Su
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
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CLASSIFICATION:
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     CTGGCTTTCCACCCAGTGACGAGGAGGATGAAGAGGGTGAGGAGTTTGTGTTTAGATTATG
                                                                                                                                            CCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTACTCACTTTTCCGCCGGCGC
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Pred. No. 0;
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919 CTOGCTTTCCACCAGGAGGATGAAAAGGATTAAAAGGATTAAAAGATTAAAAGATTAAAAGATTAAAAGATTAAAAGATTAAAAGATTAAAAGATTAAAAGATTAAAAGATTAAAAAA
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1821 GTGGAAGAGCGGTTGTGAACACAAAATGGCCTTGCTACTGTTGTCTTCCGTCCG

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1021 TATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACTTGAGCTGTAAACGCCCCAG 1080	Q	
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961 GCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGCGTCGCCAGGCTGTGGAATG 1020	γ	TOPOLOC
TACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTGAGATACACCCGGTGGTCCC 1	Db 2	SEQUENCE CHARACTERISTICS: LENGTH: 35935 base pair
901 TACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTGAGATACACCCCGGTGGTCCC 960	 О	REFERENCE/DOCKET NUMBI
841 AATIGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGTCTAGAGAATGCAATAGTAG 900 841 HAATIGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGTCTAGAGAATGCAATAGTAG 1358 1299 AATIGGCGCCTGTTATCCTGAGACGCCCGACATCACCTGTGTCTAGAGAATGCAATAGTAG 1358	B &	ATTORNEY/AGENT I NAME: Dadio, REGISTRATION N
TGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAAGACCTACCCGCCGTCCTAA 1	DЪ	
TGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAAGACCTACCCGCCGTCCTAA 840	Q	FILING DATE: 27-MAY-1994 PRIOR APPLICATION DATA:
	Db 1	APPLICATION NUMBER: US/08/379,452 FILING DATE: 26-JAN-1995 ADDITCATTON NUMBER: WO DOT/FED4/00624
721 TTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTTTTTTT	φ ξ	
661 GAAAATTATGGGCAGTGGTGATAGAGTGGTGGGTTTGGTGGTAATTTTTTTT	ł 8	CURRENT APPLICATION DATA:  APPLICATION NUMBER: US/09/409,670
1059 CAGATATTATGTGTTCGCTATATGAGGACCTGTGGCATGTTTGTCTACAGTAAGT 1118	da S	COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: PC-DOS/MS-DOS COPTWARD DE COMPATIN Delease #1 0 Version #1 20
こうしょ かっこう かっこう かっこう かっこう かっこう かっこう かっこう かっこう	 ?	; ZIF: ZZJAB-ZZJO ; COMPUTER READABLE FORM:
541 TGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCACCGGAAGAATACGGGGGACC 600	P. Q	30.
481 CTGGCTTTCCACCCAGTGACGACGAGGATGAGAGGGTGAGGAGTTTGTGTTAGATTATG 540	Db Oy	; CORRESPONDENCE ADDRESS: ; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P. ; STREET: 1737 king Street, Suite 500
TGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATCGATC	Db	; TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND CORRESPONDING ; TITLE OF INVENTION: COMPLEMENTATION LINES ; NUMBER OF SEQUENCES: 43
	Q	, APPLICANT: MEHTALI, Majid , APPLICANT: PAVIRANI, Andrea
361 CCGGTTCTCCGGAGCCGCTCACCTTTCCCGGCAGCCGAGCAGCCGAGCAGAGAGAG	Db Qy	; Patent No. 6133028 ; Patent No. 6133028 ; GENERAL INFORMATION: ; APPLICANT: IMLER, Jean-Luc
301 CCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTACTCACTTTTCCGCCGGGGC 360	dg Qy	57
ATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGGAGGCGGTTTCGCAGATTTTT	Db	3459 CTGGCCTGCACCCGCGCTGAGTTTGGCTCTAGCGATGAAGATACAGATTGAG
ATGATTTAGACGTGACGGCCCCCGAAGATCCCCAACGAGGAGGCGGTTTCGCAGATTTTTC 3	Q ·	3001 CTGGCCTGCACCCGCGCTGAGTTTGGCTCTAGCGATGAAGATACAGATTGAG 3052
181 TACTGGCTGATAATCTTCCACCTGCTAGCCATTTTGAACCACCTACCCTTCACGAACTGT 240	y da	Qy 2941 ATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGAGCTGAGGCCCGATCACTTGGTG 3000
121 ACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTGGACCAGCTGATCGAAGAGG 180	da VQ	Qy 2881 GTGCTGAGGTACGATGAGACCCGCACCAGGTGCAGACCCTGCGAGTGTGGCGGTAAACAT 2940
61 AGAGTTTTCTCCTCCGAGCCGCTCCGACACCGGGACTGAAAATGAGACATATTATCTGCC 120	dg VQ	Qy 2821 GAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTTTGACATGACCATGAAGATCTGGAAG 2880
459 CGTGTAGTGTATTTATACCCCGGTGAGTTCCTCAAGAGGCCACTCTTGAGTGCCAGCGAGT 518	Db	Db 3219 AGGGGGTGTTCCTACCTTACCAATGCAATTTGAGTCACACTAAGATATTGCTTGAGCCC 3278
IGAGTTCCTCAAGAGGCCACTCTTGAGTGCCAC	γQ	Qy 2761 AGGGGGGTGTTCCTACCTTACCAATGCAATTTGAGTCACACTAAGATATTGGTTGAGCCC 2820
Query Match 100.0%; Score 3052; DB 3; Length 35935; Best Local Similarity 100.0%; Pred. No. 0; Mismatches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Que Bes Mat	QY 2701 GCCTGGCCAGTGTTTGAGCATAACATACTGACCCGCTGTTCCTTGCATTTGGGTAACAGG 2760

	2101 AGGCCAGATTGCAAGTACAAGATCAGCAAACTTGTAAATATCAGGAATTGTTTGCTACATT 2160
GENEI	2041 TGGCTGCAGCCAGGGGATGATTTTGAGGAGGCTATTAGGGTATATGCAAAGGTGGCACTT 2100 
RESULT 8 US-09-56; Sequence	1981 TGCGCTAATGAGCTTGATCTGCTGGCGGAGAAGTATTCCATAGAGCAGCTGACCACTTAC 2040
לס לא	1921 TTTAGCTTAATGACCAGACACCGTCCTGAGTGTATTACTTTTCAACAGATCAAGGATAAT 1980 
? B &	1861 AAGGGGGTAAAGAGGGAGCGGGGGGGCTTGTGAGGCTACAGAAGGAGGCTAGGAATCTAGCT 1920
? B &	1801 GCTGAACTGTATCCAGAACTGAGACGCATTTTGACAATTACAGAGGATGGGCAGGGGCTA 1860 
} B &	1741 GCAGAGCCCATGGAACCCGAGAGCCGGCCTGGACCCTCGGGAATGAAT
}	1681 GATAATACCGACGGAGGAGCAGCAGCAGCAGGAGGAAGCCAGGCGGC
) B &	1621 GTGGAGAGCGGTTGTGAGACACAAGAATCGCCTGCTACTGTTGTCTTCCGTCCG
בא עם ג	1561 ATGGAGCGAAGAAACCCATCTGAGCGGGGGGGTACCTGCTGGATTTTCTGGCCATGCATCT 1620
) Db 49	1501 TTTTTCCACACCGGGGGCGCTGCGGCTGCTGTTGCTTTTTTGAGTTTTATAAAGGATAA 1560 
? B &	1441 TGATTCTTTGAATCTGGGTCACCAGGCGCTTTTCCAAGAGAAGGTCATCAAGACTTTGGA 1500 
? D 5	1381 AATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTTTGAAATCCTGTGGTGAGCTGTT 1440 
D 5	1321 CAĞTACCTCTTGGTTTTGGAGGTTTCTGTGGGGCTCATCCCAGGCAAAGTTAGTCTGCAG 1380 
D 64	1261 GGĆTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGCGTAACTTGCTGGAACAGAGCTCTAA 1320 
) b 4	1201 GGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCTTGGTTACATCTGACCTCATGGA 1260 
} B	1141 TGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACTTGCATGGCGTGTTAAATGGGGC 1200 
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GTGTTTGACATGACCATGAAGATCTGGAAG 3338	) GAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTTTGACATGACCATGAAGATCTGGAA	3279	밁
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TTGAGTCACACTAAGATATTGCTTGAGCCC 3278	-	3219	뮍
TTGAGTCACACTAAGATATTGCTTGAGCCC 2820	AGGGGGGTGTTCCTACCTACCAATGCAATTTGAGTCACACTAAGATATTGCTTGAGCC	2761	Ş
HACCCGCTGTTCCTTGCATTTGGGTAACAGG 3218	GCCTGGCCAGTGTTTGAGCATAACATACTGACCCGCTGTTCCTTGCATTTTGGGTAACAGG	3159	타
ACCCGCTGTTCCTTGCATTTGGGTAACAGG 2760	– ი	2701	Ş
HACCATTCACGTAGCCAGCCACTCTCGCAAG 3158		3099	рb
AACCATTCACGTAGCCAGCCACTCTCGCAAG 2700	TGCTCGGACGGCAACTGTCACCTGCTGAAGACCATTCACGTAGCCAGCC	2641	Ş
TGCGAGGACAGGGCCTCTCAGATGCTGACC 3098	GTGATTAAGCATAACATGGTATGTGGCAACTGCGAGGACAGGGCCTCTCAGATGCTGAC	3039	ᅡ
TIGCGAGGACAGGGCCTCTCAGATGCTGACC 2640		2581	ξ.
GGTTGCTTCATGCTAGTGAAAAGCGTGGCT 3038	AGGGTGCGCCACAATGTGGCCTCCGACTGTGGTTGCTTCATGCTAGTGAAAAGCGTGGCT	2979	뫄
GGTTGCTTCATGCTAGTGAAAAGCGTGGCT 2580	AGGGTGCGCCACAATGTGGCCTCCGACTGTGG	2521	Ş
PACCTTGGGTATCCTGTCTGAGGGTAACTCC 2978	TCAATTAAGAAATGCCTCTTTGAAAGGTGTACCTTTGGGTATCCTGTCTGAGGGTAACTC	2919	망
PACCTTGGGTATCCTGTCTGAGGGTAACTCC 2520	TCAATTAAGAAATGCCTCTTTGAAAGGTGTAC	2461	Ş
GGGGTGGTGTCGCCCCAAAAGCAGGGCT 2918	GGGGCTGTGCCTTTTACTGCTGCTGGAAGGGGGTGTGTCGCCCCAAAAGCA	2859	뮍
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TGTAAGCTTCTATGGGTTTAACAATACCTGTGTGGAAGCCTGGACCGATGTAAGGGTT 2858	8=	2799	뮹
TIGIGIGGAAGCCTGGACCGAIGTAAGGGIT 2400	- <u>ප</u>	2341	Ş
CAATTTTAGCGGTACGGTTTTCCTGGCCAATACCAACCTTATCCTACAC 2798	TTTACTGGCCC	2739	망
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	TCTGGGAACGGGGCCGAGGTGGAGATAGATACGGAGGATAGGGTGGCCTTTAGATGT	2619	문
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ACTTGTAAATATCAGGAATTGTTGCTACATT 2618	9 AGGCCAGATTGCAAGTACAAGATCAGCAAACTTGTAAATATCAGGAATTGTTGCTACATT	2559	망

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-09-562-919-1
Sequence 1, Application US/09562919
Patent No. 6451596
GENERAL INFORMATION:
APPLICANT: Chamberlain, Jeffrey S.
AMBLISTANDE AMBLIST

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1501 TTTTTCCACACCGGGCGCGCTGCGGCTGCTGTTGCTTTTTTGAGTTTTATAAAGGATAA 15	PTACC	٠ છ
1841 IGATIC TITEMATIC ISGITENCE CAGGCGCTTTTCCAAGAGAAGGTCATCAAGACTTTGGA	361 CCGGTTCTCCGGAGCCGCTCACCTTTCCCCGGCAGCCGAGCAGCCGGAGCAGAGAGAG	유 성
	301 CCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTACTCACTTTTCCGCCGGCGC 360	Qy db
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1321   GGCTT GGGAGGTTTTGGAAGATTTTTCTGCTGGTGAACTTGCTGGAAAGATTAGGAGGTTAAGTTAGGAAGATTTTTCTGCTGGAACTTTGCTGGAAAGATTTTAGAAGGTTAAGTTAGGAAAGATTTTTTCTGCTGGAACTTTGGTAACTTTGGAAAGATTTTAGAAGGTTAAGTTAGGAAGATTAGGAAGATTAGGAAGAA	181 TACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCACCTACCCTTCACGAACTGT 240	Db Qy
	121 ACGGAGGTGTTATTACCGAAGAATGGCCGCCAGTCTTTTGGACCAGCTGATCGAAGAGG 180	망양
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1081 GCCATIAAGGTGTAAACCTGTGATTGGGTGTGGTGTAACGCCTTTGTTTG	1 CGTGTAGTGTATTTATACCCGGTGAGTTCCTCAAGAGGCCACTCTTGAGTGCCAGCGAGT 60	B 8
	Query Match 100.0%; Score 3052; DB 3; Length 35935; Best Local Similarity 100.0%; Pred. No. 0; Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	3 W O
	MOLECULE TYPE: DESCRIPTIO SEQUENCE DESCRI 09-562-919-1	,; ;;
901 TACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTGAGATACACCCGGTGGTCCC	LENGTH: 35935 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear Db	
841 AATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGTCTAGAGAATGCAATAGTAG	TELEPHONE: (415) 705-8410  TELEPAX: (415) 397-8338  INFORMATION FOR SEQ ID NO: 1:  SEQUENCE CHARACTERISTICS:  Db	
781 TGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAAGACCTACCCGGCGTCCTAA	NAME: Ingolia, Diane E. Qy REGISTRATION NUMBER: 40,027 REFERENCE/DOCKET NUMBER: UM-02484 TELECOMMUNICATION INFORMATION: Db	
721 TITIACAGITTTGIGGTITAAAGAATTTTGTATIGTGATITTTTTTAAAAGGTCCIGTGTC	PRIOR APPLICATION DATA:  APPLICATION NUMBER: US/08/735,609  FILING DATE: 23-OCt. 1996  ATTORNEY/AGENT INFORMATION:  Db	
661 GAAAATTANGGGCAGTGGTGATAGAGTGGTGGGTTGGTGTGGTAATTTTTTTT	<b>v</b>	
601 CAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGCATGTTTGTCTACAGTAAGT	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30	
541 TGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCACCGGAGGAATACGGGGGGACC	STATE: California Qy COUNTRY: United States Of America ZIP: 94104 COMPUTER READABLE FORM:	
481 CTGGCTTTCCACCCAGTGACGACGAGGGATGAAGAGGGTGAGGAGTTTGTGTTAGATTATG	CORRESPONDENCE ADDRESS: ADDRESSEE: Medlen & Carroll, LLP STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco Db	
879 TGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATCGATC	TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS NUMBER OF SEQUENCES: 15	

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GENERAL INCORMATION:
GENERAL INCORMATION:
APPLICANT: WOLD, William
APPLICANT: TOTH, Karoly
APPLICANT: KUPPASKAMI, Mohan
APPLICANT: KUPPASKAMI, Mohan
APPLICANT: DORONIN, KONBANTIN
TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE
TITLE OF INVENTION: REPLICATION-COMPETENT IN TERT-EXPRESSING CELLS
FILE REFERENCE: 16.153-8394
CURRENT FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOMBER: US/09/956,335
CURRENT FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
LENGTH: 35978
TYPE: DNA
ORGANISM: Adenovirus
US-09-956-335-1
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ATGATTTAGACGTGACGGCCCCGAAGATCCCAACGAGGAGGCGGTTTCGCAGATTTTTC
                                                                   TACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCACCTACCCTTCACGAACTGT
                                                                                                                               ACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTGGACCAGCTGATCGAAGAGG
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	1261 GGCTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGCGTAACTTGCTGGAACAGAGCTCTAA 1320 	라 상
	1201 GGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCTTGGTTACATCTGACCTCATGGA 1260 	ρ Q
TTTACTGGCCCCAATTTTAGCGGTACGGTTTTCCTGGCCAATACCAACCTTATCCTACAC	1141 TGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACTTGCATGGCGTGTTAAATGG 	45 45
TGATAAATTATGTGGCCGGGGGTGCTTGCGCATGGACGGGGGTGGTTATTATGAATGTAAGG	1081 GCCATAAGGTGTAAACCTGTGATTGCGTGTGTGTTAACGCCTTTGTTTG	₽ <b>Q</b>
2101 AGGCCAGATTGCAAGTACAGAGTCAAACTTGTAAATTATCAGGAATTGTTGCTACATT 2160 2101 AGGCCAGATTGCAAGTACAGAGTCAGCAAACTTGTAAATTATCAGGAATTGTTACATT 2618 2559 AGGCCAGATTGCAAGGTCAAGATCAGCAAACTTTGTAAATTATCAGGAATTGTTAGATTGTACATT 2618 2161 TCTGGGAACGGCGAACGTGGAAGATAGGGATGGATGGATG	1021 TATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGAGCTTTAAGCCCCCAG 1080	용상
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3829 TITGTITGCIGAATGAGTIGAIGTAAGTITAATAAAGGGIGAGATAAIGTITAACIIGCA 3888  1183 TGGCGIGTTAAATGGGGCGGGGCTTAAAGGGTATATAATGCCGCCGIGGGCTAATCTIGGT 1242	- QQ DB	OY  43 TCTTGAGTGCCAGCGAGTAGAGTTTTCTCCTCCGACCCGGTCCGACACCGGACTGCAAAA 102
	Q D 4	Query Match 98.5%; Score 3006.8; DB 4; Length 7090; Best Local Similarity 99.9%; Pred. No. 0; Mismatches 2; Indels 0; Gaps
1003 TCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACTT 1062	S & &	; LENGTH: 7090 ; TYPE: DNA ; ORGANISM: Plasmid STK146 US-09-714-550-18
943 GATACACCCGGTGGTCCCCCCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGCG 1002	D Q	; PRIOR FILING DATE: 1999-11-23 ; NUMBER OF SEQ ID NOS: 18 ; SOFTWARE: FactSEQ for Windows Version 4.0 ; SEQ ID NO 18
883 TAGAGAATGCAATAGTAGGACAGGATAGCTGTGACTCCGGTCCTTCTAACACACCCTCCTGA 942 	p Q	; FILE REFERENCE: 50125/007002 ; CURRENT APPLICATION NUMBER: US/09/714,550 ; CURRENT FILING DATE: 2000-11-16 ; PRIOR APPLICATION NUMBER: US 60/167,439
823 ACCTACCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGTC 882	P Q	; APPLICANT: Schiedner, Gudrun ; TITLE OF INVENTION: Permanent amniocytic cell line, its ; TITLE OF INVENTION: production and use for the production of gene transfer ; TITLE OF INVENTION: vectors
763 TTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAAG 822	D Q	; Sequence 18, Application US/09714550 ; Patent NO. 6558948 ; GENERAL INFORMATION: ; APPLICANT: Kochanek, Stefan
703 GGTAATTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTTT 762 	Db Oy	RESULT 10 US-09-714-550-18
	40 53	QY 3001 CTGGCCTGCACCCGCGCTGAGTTTGGCTCTAGCGATGAAGATACAGATTGAG 3052
	, p. 75	OY 2941 ATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGAGCTGAGGCCCGATCACTTGGTG 3000
AGITIGIGITAGATIATGIGGAGCACCCCGGGCACGGITGCGGTCTIGIGATIATCACC	) B &	QY 2881 GTGCTGAGGTACGATGAGACCCGCACCAGGTGCAGACCCTGCGAGTGTGGCGGTAAACAT 2940
ATCITACCTGCCACGAGGCTGGCTTTCCACCCAGTGAGGACGAGGATGAGAGGGTGAGG	? B &	QY 2821 GAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTTTTGACATGACCATGAAGATCTGGAAG 2880
AGCCGGAGCAGAAGCCTTGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATCG	p &	Qy 2761 AGGGGGGTGTTCCTACCTTACCAATGCAATTTGAGTCACACTAAGATATTGCTTGAGCCC 2820
T-CACTIFITICGCCGGGGCCGGGTTCTCCGGAGCCCCTACCTTTCCCGGCAGCCCGAGCCCGAGCCCGAGCCCGAGCCCGAGCCCGAGCCCGAGCCCGAGCCCGAGCCCGAGCCCGAGCCCGAGCCCGAGCCCTTTCCCGGCAGCCCGAGCCGAGCCCGAGCCAGCCGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCGAGCCAGCCGAGCAGC	p 64	QY 2701 GCCTGGCCAGTGTTTGAGCATAACATACTGACCCGCTGTTCCATTTGGGTAACAGG 2760
GGTTTCGCAGATTTTTCCCGACTCTGTAATGTTGGCGGTGCAGGAAGGA	o do dy	Qy 2641 TGCTCGGACGGCAACTGTCACCTGCTGAAGACCATTCACGTAGCCAGCC
CTACCCTTCACGAACTGTATGATTTAGAACGTGACGGCCCCGGAAGATCCCAACGAGGAGG	do dy	Qy 2581 GTGATTAAGCATAACATGGTATGTGGCAACTGCGAGGACAGGGCCTCTCAGATGCTGACC 2640
163 ACCAGCIGATICANGAGATACITGCIGATAATCTTCCACCICCTAGCCATTTIGAACCAC 222	D 5	Qy 2521 AGGGTGCGCCACAATGTGGCCTCCGACTGTGGTTGCTTCATGCTAAAAAGCGTGGCT 2580
	P D	Qy 2461 TCAATTAAGAAATGCCTCTTTGAAAGGTGTACCTTGGGTATCCTGTGTGAGGGTAACTCC 2520

; SEQ ID NO 2 ; LENGTH: 35871 ; TYPE: DNA	2263 GTTATTATGAATGTAAGGTTTACTGGCCCCAATTTTAGCGGTACGGTTTTCCTGGCCAAT 2322 	å 94
CURRENT APPLICATION CONTROL OF SEQ ID SOFTMAPE: DEFENT FILING DAY	2203 GIGGCCTTTAGATGTAGCATGATAAATATGTGGCCGGGGGTGCTTGGCATGGACGGGGTG 2262	dy Qy
APPLICANT: DORON TITLE OF INVENTION TITLE OF INVENTION FILE REFERENCE: 1	2143 AGGAATTGTTGCTACATTTCTGGGAACGGGGCCGAGGTGGAGATAGAT	gy VQ
GENERAL INFORMATIO APPLICANT: WOLD, APPLICANT: TOTH, APPLICANT: KIDPA	2083 TATGCAAAGGTGGCACTTAGGCCAGATTGCAAGTACAAGATCAGCAAACTTGTAAATATC 2142	gg Qy
RESULT 11 US-09-956-335-2 ; Sequence 2, Applic ; Patent No. 6627190	2023 GAGCAGCTGACCACTTACTGGCTGCAGCCAGGGATGATTTTGAGGAGGCTATTAGGGTA 2082	gg Qy
5749	1963 CAACAGATCAAGGATAATTGCGCTAATGAGCTTGATCTGCTGCGCGCAGAAGTATTCCATA 2022 	g Qy
5689	1903 GAGGCTAGGAATCTAGCTTTAGCTTAATGACCAGACACCGTCCTGAGTGTATTACTTTT 1962 	g 9
5629	1843 GAGGATGGGCAGGGGCTAAAGGGGGTAAAGAGGGAGGGGGGGG	g Q
5569 2923	1783 ATGAATGTTGTACAGGTGGCTGAACTGTATCCAGAACTGAGACGCATTTTGACAATTACA 1842 	g &
5509	1723 CAGGCGGCGGCAGGAGCAGAGCCCATGGAACCCGAGAGCCGGCCTGGACCCTCGGGA 1782	95 V2
5449	1663 GTCTTCCGTCCGCCGGCGATAATACCGACGGAGGAGCAGCAGCAGCAGCAGGAGGAAGC 1722 	dy dy
5389 2743	1603 TTTTCTGGCCATGCATCTGTGGAGAGAGGGTTGTGAGACACAAGAATCGCCTGCTACTGTT 1662 	g Q
5329	1543 GAGTITTATAAAGGATAAATGGAGCGAAGAAACCCATCTGAGCGGGGGTACCTGCTGGA 1602 	g Q
Db 5269 CTAGTG	1483 GGTCATCAAGACTTTTGGATTTTTCCACACCGGGGGCGGCTGCGGGCTGCTGTTGCTTTTTT 1542 	A 4
5209	1423 ATCCTGTGGTGAGCTGTTTGATTCTTTGAATCTGGGTCACCAGGGGGCTTTTTCCAAGAGAA 1482 	gg Qy
	1363 GGCAAAGTTAGTCTGCAGAATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTTTGAA 1422 	문 &
5089	1303 GCTGGAACAGAGCTCTAACAGTACCTCTTGGTTTTGGAGGTTTCTGTGGGGGCTCATCCCA 1362 	g V
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Qy 2323 ACCAAC	3889 TGGCGTGTTAAATGGGGCGGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCTTGGT 3948	ďď

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                                                  CGATCACTTGGTGCTGGCCTGCACCCGCGCTGAGTTTGGCTCTAGCGATGAAGAT 5748
                                                                                                   TGGCGGTAAACATATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGAGCTG
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TIPE: MATION:

William

OTH, Karoly

OPPASWAMI, Mohan

ORONIN, KONSANCIN

NATION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE

INTION: REPLICATION-COMPETENT IN TERT-EXPRESSING CEI

CATION UMBER: US/09/956,335

IG DATE: 2001-09-19

ID NOS: 3

OTHER VECTORS

IG DATE: 201-09-19 cation US/09956335 In Ver. 2.0

CELLS

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961 GCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGCGTCGCCCAGGCTGTGGAATG 1020	901 TACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTGAGATACACCCCGGTGGTCCC 960 	841 AATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGTCTAGAGAATGCAATAGTAG 900	781 TGAACCTGAGCCTGAGCCGGAGCCAGAACCGGAGCCTGCAAGACCTACCCGGCGGTCCTAA 840	721 TTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTTTTTTAAAAGGTCCTGTGTC 780 	661 GAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTGTGGTAATTTTTT	601 CAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGCATGTTTGTCTACAGTAAGT 660 	541 TGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCACCGGAGGAATACGGGGGGACC 600	481 CTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAGGAGTTTGTGTTTAGATTATG 540	421 TGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATCGATC	361 CCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCGGAGCAGAGAGAG	301 CCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTACTCACTTTTCCGCCGGCGG 360	241 ATGATTTAGACGTGACGGCCCCGAAGATCCCCAACGAGGAGGCGGTTTCGCAGATTTTTC 300	181 TACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCACCTACCCTTCACGAACTGT 240	121 ACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTGGACCAGCTGATCGAAGAGG 180	61 AGAGTTTTCTCCTCCGAGCCGCTCCGACACCGGGACTGAAAATGAGACATATTATCTGCC 120	1 CGTGTAGTGTATTTATACCCGGTGAGTTCCTCAAGAGGCCACTCTTGAGTGCCAGCGAGT 60	Query Match 92.5%; Score 2822; DB 4; Length 35871; Best Local Similarity 96.6%; Pred. No. 0; Matches 2947; Conservative 0; Mismatches 0; Indels 105; Gaps 2;	ORGANISM: Adenovirus J9-956-335-2
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Sequence 4, Application US/08735609
Patent No. 5955360
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chamberlain, Jeffrey
APPLICANT: Amalfitano, Andrea
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LENGTH: 34303 base pairs
; TYPE: nucleic acid
; STRANDENNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic ac
DESCRIPTION: /desc = "DNA"
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ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 34303 base pairs
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Best Local Similarity
Matches 2161; Conserv
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MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735,609
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ADDRESSEE: Medlen & Carroll, LLP
------ 220 Montgomery Street, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hauser, Michael A.
APPLICANT: Kumar-Singh, Rajendra
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
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ZIP: 94104
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CITY: San Francisco
STATE: California
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                                                                    CCTCATGGAGGCTTGGGAGTTTTGGAAGATTTTTCTGCTGTGCGTAACTTGCTGGAACA
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RESULT 13  (US-08-735-609-4)  (Sequence 4, Application US/08735609)  (Patent No. 5994132)  (Patent No. 5994132	Qy  2452 RGCHGGGCTTCANTTANGANATGCCTCTTGANAGGTGTACCCTTGGGTATCCTGTGTAG  4413 AGCAGGGTTCANTTANGANATGCCTCTTTGANAGGTTACCTTGGGTATCCTGTGTAG  4413 AGCAGGGTTCANTTANGANTGCCTCTTTGANAGGTTACCTGGGTATCCTGTGTAG  Qy  2512 GGTANCTCCAGGGTGGGCCACAATGTGGCCTCCGACTGGGTATCCTGGTATCCTGTGTAAA  4513 GGTANCTCCAGGTTGGATTAAGCATTACATGTATGTGGATACCTGGGTATCCTGGTAAA  2571 AGCGTGGCTGGATTAAGCATTACACATGTTATGTGGAACCTTCCAGGACAGGGCCTCTCAG  Qy  2512 AGCGTGGCTGGATTAAGCATTACACATGTTATGTGGAACCATTCACGTAGCCAGCC

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US-08-735-609-4
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NAME: INSOLIA, Diane E.

REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3430 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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Matches 2161; Conserva
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CATGCATCTGTGGAGAGCGGTTGTGAGACACAAGAATCGCCTGCTACTGTTGTCTTCCGT
                                               GACTTTGGATTTTTCCACACCGGGGGGGCGCTGCGGCTGCTGTTGCTTTTTTTGAGTTTTTAT
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Qy 1912 AATCTAGCTTTAGCTTAATGACCAGACACCGTCCTGAGTGTATTACTTTTCAACAGATC 1971	
Db 3813 CAGGGGTAAAGAGGGGTAAAGAGGAGGCGGGGGGCTTGTGAGGCTACAGAGGAAGGCTAGG 3872	MOLECULE TYPE DESCRIPTION S-09-315-372-4
1060	STRANDEDNESS:
1792 GTACAGGTGGCTGAACTGTATCCAGAACTGAGACGCATTTTGACAATTACAGAGGATGGG	SEQUENCE CHARACTERISTICS: LENGTH: 34303 base pairs
Qy 1732 GCGGCAGGAGCCCATGGAACCCGAGAGCCGGCCTGGACCCTCGGGAATGAAT	TELECOMMUNICATION INFORMATIO TELEPHONE: (415) 705-8410 TELEFAX: (415) 397-8338 INFORMATION FOR SEO ID NO: 4:
Qy 1672 CCGCCCGGCGATAATACCGACGAGGAGCAGCAGCAGCAGCAGGAGGAAGCCAGGCGGC	; ATTORNEY/AGENT INFORMATION: ; NAME: INGOLIA, Diane E. ; REGISTRATION NUMBER: 40,027 ; REFERENCE/DOCKET NUMBER: UM-02484
Qy 1612 CATGCATCTGTGGAGAGGGGTTGTGAGACACAAGAATCGCCTGCTACTGTTGTCTTCCGT 1671	
Qy 1552 AAAGGATAAATGGAGCGAAGAAACCCATCTGAGCGGGGGGGTACCTGCTGGATTTTCTGGC 1611	SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/09/315,372 FILING DATE:
Qy 1492 GACTITGGATITTTCCACACCGGGGCGCGCTGCGGCTGCTGTTTTTTTGAGTITTAT 1551	COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk  COMPUTER: IBM PC compatible  OPERATING SYSTEM: PC-DOS/MS-DOS
Qy 1432 TGAGCTGTTTGATTCTTTGAATCTGGGTCACCAGGCGCTTTTCCAAGAGAAGGTCATCAA 1491	CITY: San Francisco ; STATE: California ; COUNTRY: United States Of America 7.TP: 94104
Qy 1372 AGTCTGCAGAATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTTTGAAATCCTGTGG 1431	N)
Qy 1312 GAGCTCTAACAGTACCTCTTGGTTTTGGAGGTTTCTGTGGGGCTCATCCCAGGCAAAGTT 1371	APPLICANT: Hauser, Michael A. APPLICANT: Kumar-Singh, Rajendra APPLICANT: Kumar-Singh, Rajendra APPLICANT: Hartigan-O'Connor, Dennis J. TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
Qy 1252 CCTCATGGAGGCTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGGGTAACTTGCTGGAACA 1311	Patent No. 6057158  GENERAL INFORMATION: APPLICANT: Chamberlain, Jeffrey S. APPLICANT: Amalfitano, Andrea
Qy 1192 AAATGGGGGGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCTTGGTTACATCTGA 1251	RESULT 14 US-09-315-372-4 ; Sequence 4, Application US/09315372
Qy 1132 TGAATGAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACTTGCATGGCGTGTT 1191	Qy 3052 G 3052 Db 5013 G 5013
Qy 1072 ACGCCCCAGGCCATAAGGTGTAAACCTGTGATTGCGTGTGGGTTAACGCCTTTGTTTG	Oy 2992 CACTTGGTGCTGGCCTGCACCCGCGCTGAGTTTGGCTCTAGCGATGAAGATACAGATTGA 3051
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Query Match 70.8%; Score 2161; DB 3; Length 34303; Best Local Similarity 100.0%; Pred. No. 0; Matches 2161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Oy 2752 GGTAACAGGAGGGGGGGTGTTCCTACCTTACCAATGCAATTTGAGTCACACTAAGATATTG 2811

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patent No. 6663622
; GENERAL INFORMATION:
APPLICANT: Chamber;
APPLICANT: Amalfit;
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US-09-244-752-4
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US-09-244-752-4
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Best Local Similarity
Matches 2161; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hauser, Michael A.
APPLICANT: Kumar-Singh, Rajendra
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 34303 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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CITY: San Francis
STATE: California
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ZIP: 94104
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Search completed: October 28, 2005, 09:05:32 Job time : 528 secs

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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
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## SUMMARIES

4484	Remult No.
305 305 305 305 205 205 205 205 205 205 205 205 205 2	Query Score Match Length DB ID
11000.0	Query
3052 9905 32802 35935 35935	Length
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100.0 3052 26 US-11-070-890-33 100.0 9905 24 US-10-731-961-3 100.0 32802 21 US-10-766-307A-3 100.0 35935 9 US-09-725-720-43 100.0 35935 9 US-09-782-378A-4	ID
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## ALIGNMENTS

Query Match Best Local Similarity	; LENGTH: 3052 ; TYPE: DNA ; ORGANISM: Human Adenovirus Type 5 ; FEATURE: ; OTHER INFORMATION: Nucleotides 45 US-11-070-890-33	CURRENT APPLICATION NUMBER: US/11/070,890 CURRENT FILING DATE: 2005-03-04 PRIOR APPLICATION NUMBER: 09/549,463 PRIOR FILING DATE: 2000-04-14 PRIOR APPLICATION NUMBER: 60/129,452 PRIOR FILING DATE: 1999-04-15 NUMBER OF SEQ ID NOS: 33 SOFTWARE: PATENTIN VERSION 3.1 SEQ ID NO 33	RESULT 1  US-11-070-890-33  Sequence 33, Application US/11070890  Publication No. US20050170463A1  GENERAL INFORMATION: APPLICANT: Bout, Abraham APPLICANT: Boytelten, Jan-Dirk TITLE OF INVENTION: RECOMBINANT PRO TITLE OF INVENTION: COMPRISE NUCLE
100.0%;	ovirus Typ lucleotides	TUMBER: US/ 2005-03-0 1BER: 09/54 100-04-14 1BER: 60/12 199-04-15 133	on US/1107 0170463A1 ham Lacombinant
Score 3052; DB 26; Length 3052; Pred. No. 0;	TYPE: DNA TYPE: DNA ORGANISM: Human Adenovirus Type 5 FEATURE: OTHER INFORMATION: Nucleotides 459-3510 of Human Adenovirus Type 5 1-070-890-33	/11/070,890 04 49,463 29,452	ULT 1 11-070-890-33 11-070-890

	1021 TATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACTTGAGCTGTAAACGCCCCAG 1080	4c 6y
	961 GCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGCGTCGCCAGGCTGTGGAATG 1020	B 8
TGGCTGCAGCCAGGGGATGATTTTGAGGAGGCTATTAGGGTATATGCAAAAGGTGGCACTT	901 TACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTGAGATACACCCGGTGGTCCC 960	g &
TGCGCTPAPTGACCTTGACCTGCCTGGCGGAAGTATTCCATAGAGCAGCTGACCACCTTAC	841 AATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGTCTAGAGAATGCAATAGTAG 900	Qу
ANGGGGGTAAAGAGAGAGAGAGGGGCTTGTGAGGGTACAAGAAGAGATCAAGGATTTTTGAAGAGGAAGGA	781 TGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAAGACCTACCCGCCGTCCTAA 840	Qy db
1801 GCIGARCIGIAICCAGAACIGAGACAGAIIIICACAAIIACAGAGAIGGGCAGGGCCIA 1800   1801 GCIGAACIGIAICCAGAACIGAGACAGAIIIICAGA   1800   1801 GCIGAACIGAGACGCAGAGCGCATTTTGACAATTACAGAGGATGGGCAGGGGCTA 1860   1861 NACGGGGTAAAGGAGGGGCGCTA 1860   1861 NACGGGGTAAAGGAAGGGGGCTA 1860   1861 NACGGGGTAAAGGAAGGGGGCTAAGGAAGGGGGCTAAGGAAGG	721 TTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTTTTTAAAAGGTCCTGTGTC 780	g &
1/41 GCAGAGCCCATGGAACCCGAGAGCCGGCCTGGACCCTCGGGAATGAAT	661 GAAAATTATGGGCAGTGGTGATAGAGTGGTGGGTTTGGTGGTAATTTTTTTT	g &
	601 CAGATATTATGTGTCGCTTTGCTATATGAGGACCTGTGGCATGTTTTGTCTACAGTAAGT 660	g Q
1681 GATAATACCGACGGACGAGCAGCAGCAGCAGGAGGAAGCCAGGCGCGGCG	541 TGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCACCGGAGGAATACGGGGGACC 600	B 8
1531 GTGGAGGGGTTGTGGAGAAGAATCGCCTGCTGCTGCTTGCT	481 CTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAGGAGTTTGTGTTAGATTATG 540	db db
	421 TGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATCGTACCTGCCACGAGG 480	gy Qy
	361 CCGGTTCTCCGGAGCCGCTCACCTTTCCCGGCAGCCGAGCAGCCGGAGCAGAGAGCCT 420	g V
1381 AATTTAAGGAGGATTACAAGTTGGGAAATTTGAAGAAGAAGGTTTTTGAAGAAGTCATCAAGAGACTTTTGGAAGAGACTTTTTGAAGAAGTTCATCAAGAGACTTTTTTTT	301 CCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTACTCACTTTTCCGCCGGCGC 360	ρ <b>જ</b>
	241 ATGATTTAGACGTGACGGCCCCGGAAGATCCCAACGAGGAGGCGGTTTCGCAGATTTTTC 300   Db   241 ATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGGAGCGGTTTCGCAGATTTTTC 300   Db   Db   Db   Db   Db   Db   Db	d VQ
	181 TACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCACCTACCCTTCACGAACTGT 240	유 <b>상</b>
	121 ACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTGGACCAGCTGATCGAAGAGG 180	B 8
	61 AGAGTTTTCTCCTCCGAGCCGCTCCGACACCCGGGACTGAAAATGAGACATATTATCTGCC 120	당 왕
	1 CGTGTAGTGTATTTATACCCGGTGAGTTCCTCAAGAGGCCACTCTTGAGTGCCAGCGAGT 60	유 상
1081 GCCATAAGGTGTAAACCTGTGATTGCGTGTGTGGTTAACGCCTTTGTTTG	Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Mat

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RESULT 2
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Sequence 3, Application US/10731961
Publication No. US20050130306A1
GENERAL INFORMATION:
APPLICANT: Voeliny, Richard W.
TITLE OF INVENTION: VIRAL VECTORS WHOSE REPLICATION AND, OPTIONALLY, PASSENGER TITLE OF INVENTION: ARE CONTROLLED BY A GENE SWITCH ACTIVATED BY HEAT IN THE PILLE OF INVENTION: OR ABSENCE OF A SMALL MOLECULE REGULATOR
FILLE REPERENCE: Replicating virus
CURRENT APPLICATION NUMBER: US/10/731,961
CURRENT FILING DATE: 2003-12-10
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PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/191,580
PRIOR APPLICATION NUMBER: 60/191,580
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 4
SOPTWARE: Patentin version 3.3
SEQ ID NO
LENGTH: 9905
TYPE: DNA
ORGANISM: Artificial
PEATURE:
OTHER INFORMATION: pXC1 plasmid
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                                                                 TTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTTTTTTAAAAGGTCCTGTGTC
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Pred. No. 0;
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Sequence 3, Application US/10766307A
Sequence 3, Application US/10766307A
Publication No. US20040202663A1
GENERAL INFORMATION:
APPLICANT: Shanghai Sunway Biotech Co., LTD.
TITLE OF INVENTION: Treatment for Metastatic Car
FILE REFERENCE: 121300.00003
CURRENT APPLICATION UNMBER: US/10/766,307A
CURRENT FILING DATE: 2004-01-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 32802
TYPE: DNA
CORGANISM: Adenovirus
US-10-766-307A-3
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RESULT 4
US-09-725-720-43
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Best Local Similarity
Matches 3052; Conser
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Patent No. U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: United States
ZIP: 22314-2756
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/725,720
                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: (
INFORMATION FOR SEQ ID NO: 433
SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93 064
PILING DATE: 28-MAY-1993
ATTORNEY AGENT INFORMATION:
NAME: Dadio, Susan M.
REGISTRATION NUMBER: 40,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: IMLER, Jean-Luc
APPLICANT: MEHTALI, Majid
APPLICANT: PAVIRANI, Andrea
TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES AND
TITLE OF INVENTION: COMPLEMENTATION LINES
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                TYPE: nucleic ac
STRANDEDNESS: si
TOPOLOGY: linear
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CITY: Alexandria
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US20010049136A1
                   ACGGAGGTGTTATTACCGAAGAAATGGCCGCCGCCAGTCTTTTGGACCAGCTGATCGAAGAGGG
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                                                                       AGAGTTTTCTCCTCCGAGCCGCTCCGACACCGGGACTGAAAATGAGACATATTATCTGCC
                                                                                             AGAGTTTTCTCCTCCGAGCCCGCTCCGACACCCGGGACTGAAAATGAGACATATTATCTGCC
                                                                                                                                               CGTGTAGTGTATTTATACCCCGGTGAGTTCCTCAAGAGGCCACTCTTGAGTGCCAGCGAGT
                                                                                                                                                                        CGTGTAGTGTATTTATACCCGGGTGAGTTCCCTCAAGAGGCCACTCTTGAGTGCCAGCGAGT
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1737 King Street, Suite 500
                                                                                                                                                                                                                     100.0%; Score 3052; ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches
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QY 2341 GGTGTAAGCTTCTATGGGTTTAACAATACCTGTGTGGAAGCCTGGACCGATGTAAGGGTT 2400	Db 2739 TTTACTGGCCCAATTTTAGCGGTACGGTTTTCCTGGCCAATACCAACCTTATCCTACAC 2798	2679 ATGATAAATATGTGGCCGGGGGTGCTTGGCATGGACGGGGTGGTTATTATGAATGTAAGG	Db 2619 TCTGGGAACGGGCCGAGGTGGAGATAGATACGGAGGATAGGTGGCCTTTAGATGTAGC 2678  Qy 2221 ATGATAAATATGTGGCCGGGGGTGCTTGGCACGGGGTGGTTATTATGAATGTAAGG 2280	Db 2559 AGGCCAGATTGCAAGATCAGAATATCAGGAATTGTTGCTACATT 2618  Qy 2161 TCTGGGAACGGGCCGAGGTGAGATAGATACGGAGGATAGGGTGGCCTTTAGATGTAGC 2220	Db 2499 TGGCTGCAGGCAGGGGATGATTTTGAGGAGGGGTATATGAGGAAAGGTGGCACTT 2558  Qy 2101 AGGCCAGATGCAAGTACAAGATCAGGAAACTTGTTAAATATCAGGAATTGTTGCTACATT 2160	QY 1981 TGCGCTRATGAGCTTGATCTGCTGGCGCGAGAGTATTCCATAGAGCAGCTGACCACTTAC 2040	1921 TTTAGCTTAATGACCAGACACCGTCCTGAGTGTATTACTTTTCAACAGATCAAGGATAAT	AAGGG       AAGGG	Qy 1801 GCTGAACTGTATCCAGAACTGAGACGCATTTTGACAATTACAGAGGATGGGCAGGGGCTA 1860	QY 1741 GCAGAGCCCATGGAACCCGAGAGCCGGCCTGGACCCTCGGGAATGAAT	81 GATAAT        39 GATAAT	GTGGAGAGCGGTTGTGAGACACAAGAATCGCCTGCTACTGTTGTCTTCCGTCCG	Qy 1561 ATGGAGCGAAGAAACCCATCTGAGCGGGGGGTACCTGCTGGATTTTTCTGGCCATGCATCT 1620	Qy 1501 TTTTTCCACACCGGGCGCGCTGCGGCTGCTGTTGCTTTTTTGAGTTTTATAAAGGATAA 1560		QY 1381 AATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTTTGAAATCCTGTGGTGAGCTGTT 1440	CAGTACCTCTTGGTTTTGGAGGTTTCTGTGGGGCTCATCCCAGGCAAAGTTAGTCTGCAG	1/19 GGCTTGGGAGGTTTTGGAAGATTTTTCTGCTGTGCGTAACTTGCTGGAACAGAGCTCTAA

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RESULT 5

US-09-782-378A-4
; Sequence 4, Application US/09782378A
; Patent No. US20020102731A1
; GENERAL INFORMATION:
APPLICANT: Hearing, Patrick
APPLICANT: Sandalon, Ziv
APPLICANT: Sandalon, Ziv
APPLICANT: Gnatenko, Dmitri
TITLE OF INVENTION: Adenoviral Vectors
FILE REFERENCE: STONYB-04970
; CURRENT APPLICATION NUMBER: US/09/782,378A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/237,747
PRIOR APPLICATION NUMBER: 60/237,747
PRIOR APPLICATION NUMBER: 60/237,747
; PRIOR APPLICATION NUMBER: 60/237,747
; PRIOR PATELING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; SEQ ID NO 4
; SEQ ID NO 4
; ORGANISM: Human adenovirus type 5
US-09-782-378A-4
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 Score 3052;
Pred. No. 0;
               BB
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               Length 35935;
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RESULT 6  US-09-782-378A-5  ; Sequence 5, Application US/09782378A  ; Patent No. US20020102731A1  ; GENERAL INFORMATION:  APPLICANT: Hearing, Patrick  ; APPLICANT: Bahou, Wadie  ; APPLICANT: Sandalon, Ziv  ; APPLICANT: Gnatenko, Dmitri  ; TITLE OF INVENTION: Adenoviral Vectors  ; FILE REFERENCE: STONYB-04970  ; CURRENT APPLICATION NUMBER: US/09/782,378A	Dy 2111 TCTGGGANCGGGGCCGAAGTTGGATACGATAGGATAGGAT

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CTGGCCTGCACCCGCGCTGAGTTTGGCTCTAGCGATGAAGATACAGATTGAG
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APPLICATION NUMBER: FR 93 06482
APPLICATION NUMBER: FR 93 06482
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Dadio, Susan M.
REGISTRATION NUMBER: 40,373
REFERENCE/DOCKET NUMBER: 029395-002
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Publication No. US20030170885A1
GENERAL INFORMATION:
APPLICANT: IMLER, Jean-Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 3052; Conserv
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CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS,
STREET: 1737 King Street, Suite 500
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MEHTALI, Majid
PAVIRANI, Andrea
TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/739,007
FILING DATE: 19-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTACTCACTTTTCCGCCGGCGC
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                                                                                  ATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGGAGGCGGTTTCGCAGATTTTTC 300
                                                                                                                                                            TACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCACCTACCCTTCACGAACTGT 240
                                                                                                                                                                                                                  ACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTGGACCAGCTGATCGAAGAGG
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2919 TCAATTAAGAAATGCCTCTTTGAAAGGTGTACCTTGGGTATCCTGTCTGAGGGTAACTCC 2978	1381 AATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTTTGAAATCCTGTGGTGAGCTGTT 1440   Line   Line	유 성
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271 GIGGGGTTGTTTTTACTGCTGGAAGCGTGGTGTGGACCCGAAAAGGGGT 2460	1261 GGCTTGGGAAGATTTTTCTGCTGTGCGTAACTTGCTGGAACAGAGCTCTAA 1320	B 8
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AGGCCAGATTGCAAGTTCAAGATCAGCAAACTTGTAAATATCAGGAATTGTTGCTACATT 	1021 TATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGAGCTGTAAACGCCCCAG 1080	පි රි
TGGCTGCAGCCAGGGGATGATTTTGAGGGAGGCTATTAGGGTATATGCAAAGGTGGCACTT	961 GCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGCGCCAGGCTGTGGAATG 1020	당 <b>상</b>
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TETRAGETIANTSACCAGACACCGTCCTGAGTGTATTACTTTTCAACAGATCAAGGATAAT  TITAGCTTAATGACCAGACACCGTCCTGAGTGTATTACTTTTCAACAGATCAAGGATAAT  TITAGCTTAATGACCAGACACCGTCCTGAGTGTATTACTTTTCAACAGATCAAGGATAAT  TOTGGTAATGACCAGACACCGTCCTGAGTGTATTACTTTTCAACAGATCAAGGATAAT	841 AATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGTCTAGAGAATGCAATAGTAG 900	д Q
AAGGGGTAAAGGAAGCGGGGGGGCTTGTGAGGCTACAGAGGCTAGGAATCTAGCT	781 TGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAAGACCTACCCGCCGTCCTAA 840	ρ <b>જ</b>
	721 TTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTTTTTAAAAGGTCCTGTGTC 780	B &
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	QY 1201 GGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCTTGGTTACATCTGACCTCATGGA	Qy 121 ACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTGGACCAGCTGATCGAAGAGG
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CONTRIBUTION CONTRIBUTION 2790  De 39 TRANSPIRACEORCECTOCOMA 2790  De 301 CONTRIBUTION CONTRIBUT	60 kg 1539	Qy 1 CGTGTAGTGTATTTATACCCGGTGAGTTCCTCAAGAGGCCACTCTTGAGT
TECHNANCCONTROLOGICACTOR 2700  DE SON CONTROLOGICA 2700  DE SON CONTRO	Qy 1021 i Db 1479 Gaps 0; C: 1081	Score 3052; DB 19; Length Pred. No. 0; Mismatches 0; Indels
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CRANGECCAPTEACGAGGCACCTTCCCAMA 2158   Oy   CCGACTCTTANTTTCCCAGAGAGCATTTCCCAGAGACCCCTTACTTCCCAGAGACCCCTTTACTTCCCAGAGACCCCTTTACTTCCCAGAGACCCCTTTACTTCCCCGCGCCCCCCATACTTCCCCCCGAGACCCCCTTACTTCCCCCGCCCCCCCC	901 1359	SOFTWARE: PatentIn Ver. 2. SEQ ID NO 12 LENGTH: 35935 TYPE: DNA
TOTANCHICACTICACTACCANCACTCTCCANA 2700  DE SATATTANACGTACCACCACTCTCCANA 3158  OY  TOTANACCACCACTCTCCANACTTCCCANACATCACTACCACCACTTTCCCACCACCACCACCACCACC	841 1299	CURRENT FILING DATE: 2002-: PRIOR APPLICATION NUMBER: 6 PRIOR FILING DATE: 2001-10-1 NUMBER OF SEO ID NOS: 15
CGARGECCATTCAGGRAGCACCCCCGAAGACCTTTCCACAAGACGATTTCCACAAGATTTTCCCCGAAGACCATTCAGGRAGCATTCAGGRAGCATTCAGGRAGCATTCCACAGACGATTCCACTTTTCCCCCCGCCAGAAACCTTTAGGGRAACAGATTCCACTTTCCCCCCCCCC	781 1239	APPLICANT: AGUILAR-CORDOVA, CARLOS ESTUARDO TITLE OF INVENTION: CHIMERIC VIRAL VECTORS FOR GENE FILE REFERENCE: 13087-105 26 1910/264 839
Db 699 ATGATTTAGACGTCCCGAAAGATCCCAACGAGAGAGAGGCTTTCCCACGAGATTTTC	721 1179	വന
2700  Db 699 ATGATTTAGACGTGACGACGAAGATCCCAACGAAGAGGCGGTTTCCCAGATTTTC 3158  Qy 301 CCGACTCTGTAATGTTGGCGTGCAGGAAGGGATTGACTTACTCACTTTTCCGCCGGCGC 2760  Db 759 CCGACTCTGTAATGTTGGCGTGCAGGAAGGGATTGACTTACTCACTTTTCCGCCGGCGC 3218  Qy 361 CCGGTTCTCCGGAAGCGCTCACCTTTCCCGGCAGCAGCAGCAGCAGCAGCAGCAGAGAGCCT [	Qy 661 Db 1119	Db 3459 CTGGCCTGCACCCGCGCTGAGTTTGGCTCTAGCGATGAAGATACAGATTGAG RESULT 8
2700  Db 699 ATGATTTAGACGTGACGACGAAGATCCCAACGAGGAGGCGTTTCGCAGATTTTC  3158  Qy 301 CCGACTCTGTAATGTTGGCGGTGCAGGAAGGCGTTCACTTTTCCGCCGGCGCGCGC	Db 1059	3001
2700  Db 699 ATGATTTAGACGTGACGACGAAGATCCCAACGAGGAGGCGTTTCGCAGATTTTC  3158  Qy 301 CCGACTCTGTAATGTTGGCGGTGCAGGAAGGCGTTTCGCACGTTTTCCGCCGGCGGCGCGCGGTGCAGGAAGGCGTTTACTCACTTTTCCGCCGGCGGCGCGCGGTGCAGGAAGGGATTGACTTACTCACTTTTCCGCCGGCGGCGCGCGAGCAGGAAGGGATTGACTTACTCACTTTTCCGCCGGCGGCGCGCGGCGGGAGAGGGATTGACTTACTCACTTTTCCGCCGGCGGCGGGCG	3000 Db 999	Qy 2941 ATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGAGCTGAGGCCCGA
2700  Db 699 ATGATTTAGACGTGACGGCCCCGAAGATCCCAACGAGGAGGCGGTTTCCCAGATTTTC  3158  Qy 301 CCGACTCTGTAATGTTGGCGTGCAGGAAGGAGGCGTTTCCGCCGGCGC  2760  Db 759 CCGACTCTGTAATGTTGGCGTGCAGGAAGGGATTGACTTACTCACTTTTCCGCCGGCGC  2760  Db 759 CCGACTCTGTAATGTTGGCGTGCAGGAAGGGATTGACTTACTCACTTTTCCGCCGGCGC  3218  Qy 361 CCGGTTCTCCGGAGCCGTCACCTTTCCCGGAGCAGCAGCAGAGAGCCT  3218  Qy 461 CCGGTTCTCCGGAGCCCTCACCTTTCCCGGCAGCCAGAGCAGAGAGCCT  3278  Qy 421 TGGGTTCCGGAGCCCTCAAACCTTGTACCGGAGCAGCCGGAGCAGAGAGCCT  3278  Qy 481 CTGGGTTTCCAACCGTTTACTCAAACCTTTGTACCGAAGGTGATCTTACCTGCCACGAGG  3338  Qy 481 CTGGGTTTCCACCAGAGGAGGAGGAGGAGGAGTTTGTGTTAGATTATGG  1	2940 pb 939 3398 Qy 541	QY 2881 GTGCTGAGGTACGATGAGACCCGCACCAGGTGCAGACCCTGCGAGTGTGGCGGTAAACAT
G 2700  Db 699 ATGATTTAGACGGCCCCGAAGATCCCAACGAGGAGGCGGTTTCGCAGATTTTCG G 3158  Qy 301 CCGACTCTGTAATGTTGGCGGAGAGGGAGTTGACTTACTCACTTTTCCGCCGGCGG G 2760  Db 759 CCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTACTCACTTTTCCGCCGGCGG G 2718  Qy 361 CCGGTTCTCCGGAGCCGCTCACCTTTCCCGGAGCAGAGAGCCT G 3218  Qy 361 CCGGTTCTCCGGAGCCGCTCACCTTTCCCGGAGCAGAGAGCCT G 3278  Qy 421 TGGGTCCGGTTCTATGCCAAACCTTGTACCGGAGCAGACCAGAGAGAG	3338 Qy 481	3279
2700 Db 699 ATGATTTAGACGTGACGGCCCCGAAGATCCCAACGAGGAGGCGGTTTCGCAGATTTTTC  3158 Qy 301 CCGACTCTGTAATGTTGGCGGTGCAGGAAGGAGGAGTTGACTTACTCACTTTTCCGCCGGCGC  2760 Db 759 CCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTACTCACTTTTCCGCCGGCGC  2760 Db 759 CCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTACTCACTTTTCCGCCGGCGC  2760 Db 759 CCGACTCTCCGGAGCCGCCTCACCTTTCCCGGAGCAGCAGCAGAGAGAG	C 3278 Oy 421	3219
2700 Db 699 ATGATTTAGACGTGACGGCCCCGAAGATCCCAACGAGGGGGGGTTTCGCAGATTTTTC 3158 Qy 301 CCGACTCTGTAATGTTGGCGGTGCAGGAAGGATTGACTCACTTTTCCGCCGGCGC	2820 Db 819	Qy 2761 AGGGGTGTTCCTACCTTACCAATGCAATTTGAGTCACACTAAGATATT
2700 Db 699 ATGATTTAGACGTGACGGCCCCGAAGATCCCAACGAGGAGGCGGTTTCGCCAGATTTTTC 3158 Qy 301 CCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTACTCACTTTTCCGCCGGCGC	2760 Db 759	2701 G
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2640 Db 639 3098 Qy 241	2640 Db 639 3098 Qy 241	CY 2581 GIGATIANGCATIANCATIGGTATGTIGGCAACTGCGAGGACAGGGCCTCTCAGATGCTGAG
T 2580  Db 579 ACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTGGACCAGCTGATCGAAGAGG  T 3038  Qy 181 TACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCACCTTACCCTTCACGAACTGT	2580 Db 5 3038 Qy 1	2521 2979

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CAAGTACAAGATCAGCAAACTTGTAAATATCAGGAATTGTTGCTACATT 2160 	2101 AGGCCAGATTGCAAGTACAAGAT 
CCAGGGGATGATTTTGAGGAGGCTATTAGGGTATATGCAAAGGTGGCACTT 2100	2041 TGGCTGCAGCCAGGGGATGATTT
CGCTAATGAGCTTGATCTGCTGGCGCAGAAGTATTCCATAGAGCAGCTGACCACTTAC 2040	1981 TGCGCTAATGAGCTTGATCTGCT
CTTAATGACCAGACACCGTCCTGAGTGTATTACTTTTCAACAGATCAAGGATAAT 1980 	1921 TTTAGCTTAATGACCAGACACCG
TTGTGAGGCTACAGAGGAAGCTAGGAATCTA	1861 AAGGGGGTAAAGAGGGAGCGGGGGGGGGGGGGGGGGGGG
CATTTTGACAAT	1801 GCTGAACTGTATCCAGAACTGAGACC 
:ggcctggaccctcgggaatgaatgttgtacag 	1741 GCAGAGCCCATGGAACCCGAGAGCC
GCAGCAGCAGGAGGAAGCCAGGCGGCGGCGGCAGGA 1740	1681 GATAATACCGACGGAGGAGCAGCAG
AAGAATCGCCTGCTACTGTTGTCTTCCGTCCGCCCGGC 1680	1621 GTGGAGAGCGGTTGTGAGACACA                 2079 GTGGAGAGCGGTTGTGAGACACA
CCATCTGAGCGGGGGTACCTGCTGGATTTTCTGGCCATGCATCT 1620	1561 ATGGAGCGAAGAAACCCATCTGA                   2019 ATGGAGCGAAGAAACCCATCTGA
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ACAAGTGGGAATTTGAAGAGCTTTTGAAATCCTGTGGTGAGCTGTT 1440 	381 AATTAAGGAGGATT 
TCTGTGGGGCTCATCCCAGGCAAAGTTAGTCTGCAG 1380	1321 CAGTACCTCTTGGTTTTGGAGGT
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RESULT 9
US-10-432-889-1
Sequence 1, Application US/10432989
Publication No. US20040097455A1
GENERAL INFORMATION:
APPLICANT: Aguilar Cordova, Estuardo
TITLE OF INVENTION: Recombinant viral and non-viral vectors
TITLE OF INVENTION: containing the human gene of the urokinase plasminogen
TITLE OF INVENTION: types of fibrosis such as hepatic, renal, pulmonary,
TITLE OF INVENTION: bancreatic, heart fibrosis as well as hypertrophic scars
FILLE REFERENCE: 558-035-994(205/19071)
CURRENT APPLICATION NUMBER: US/10/432,989
CURRENT APPLICATION NUMBER: US/10/432,989
PRIOR APPLICATION NUMBER: PCT/MX00/00050
PRIOR APPLICATION NUMBER: MX011713
PRIOR APPLICATION NUMBER: MX011713
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 13
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 35935
TYPE: DNA

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	S & &	721 TITTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTTTTTAAAAGGTCCTGTGTC 780 	B 8
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AA11ANGGAGATIACAAG1GGGAA11IGAAGAGCTIIIGAAA CCIGIGGIGAGCIGII 	} B &	301 CCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTACTCACTTTTTCCGCCGGCGC 360 	ß 8
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	?	Query Match 100.0%; Score 3052; DB 19; Length 35935; Best Local Similarity 100.0%; Pred. No. 0; Matches 3052; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Que Bes Mat
GCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGCGTCGCCAGGCTGTGGAATG	? B	ORGANISM: Human adenovirus type 5 0-432-989-1	, o

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RESULT 10
US-10-766-307A-4
; Sequence 4, Application US/10766307A
; Publication No. US20040202663A1
; GENERAL INFORMATION:
; APPLICANT: Shanghai Sunway Biotech (
; TITLE OF INVENTION: Treatment for Mo.
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; CURRENT APPLICATION NUMBER: US/10/766,307A
; CURRENT FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 35935
; TYPE: DNA
; ORGANISM: addenovirus
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	1681 GATAATACCGACGGAGGAGCAGCAGCAGGAGGAGGAGGAGGCAGGCGGC	B 8
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1981 TGCGCTAATGAGCTTGATCTGCTGGCGCAGAAGTATTCCATAGAGCAGCTGACCACTTAC 2040	ANTGGCGCCTGCTATCCTGAGACGCCCCGACATCACCTGTGTCTAGAGAATGCAATAGTAG 1	) B

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Sequence 8, Application US/10492178

| Sequence 8, Application No. US20040247615A1
| GENERAL INFORMATION:
| APPLICANT: Emini, Emilio A.
| APPLICANT: Emini, Emilio A.
| APPLICANT: Emini, Emilio A.
| APPLICANT: Emini, Emini A.
| APPLICANT: Lahm, Armin
| APPLICANT: Lahm, Armin
| APPLICANT: Lohm, Armin
| APPLICANT: Lolloca, Stefano
| APPLICANT: Colloca, Stefano
| APPLICANT: Colloca, Stefano
| TITLE OF INVENTION: HEPATITIS C VIRUS VACCINE
| FILE REFERENCE: ITRO015YP
| CURRENT APPLICATION NUMBER: US/10/492,178
| CURRENT APPLICATION NUMBER: BOUNDER: POPERIOR APPLICATION NUMBER: PCT/US02/32512
| PRIOR APPLICATION NUMBER: 60/363,774
| PRIOR APPLICATION NUMBER: 60/363,774
| PRIOR APPLICATION DATE: 2002-03-13
| PRIOR APPLICATION DATE: 2001-10-11
| NUMBER OF SEQ ID NOS: 17
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 8
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; LENGTH: 35935
; TYPE: DNA
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US-10-492-178-8
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                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Luzzago, Alessandra
APPLICANT: Cortese, Riccardo
APPLICANT: Collos, Stefano
IITLE OF INVENTION: HEPATITIS C VIRUS VACCINE
FILE REFERENCE: ITRO015YP
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US/10/492,178
CURRENT FILING DATE: 2004-01-07
PRIOR RPILICATION NUMBER: FO/363,774
PRIOR RPILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 60/363,774
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 60/365
PRIOR PILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO
SEQ ID NO
LENGTH: 35935
TYPE: DNA
ORGANISM: Adenovirus serotype 5
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Publication No. US20040247615A1
GENERAL INFORMATION:
APPLICANT: Emini, Emilio A.
APPLICANT: Kaslow, David C.
APPLICANT: Kaslow, David C.
APPLICANT: Shiver, John W.
APPLICANT: Nicosia, Alfredo
APPLICANT: Luzzago, Alessandra
APPLICANT: Lores Alessandra
APPLICANT: Cortege, Riccardo
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                                                                                                                                   AGAGTTTTCTCCTCCGAGCCGCTCCGACACCGGGACTGAAAATGAGACATATTATCTGCC
                                                                                                                                                                                                         CGTGTAGTGTATTTATACCCCGGTGAGTTCCTCAAGAGGCCACTCTTGAGTGCCAGCGAGT
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Qy 2041 TGGCTGCAGCCAGGGGATGATTTTGAGGAGGCTATTAGGGTATATGCAAAGGTGGCACTT
Qy 1921 TTTAGCTTAATGACCAGACACCGTCCTGAGTGTATTACTTTTCAACAGATCAAGGATAAT
Qy 1801 GCTGAACTGTATCCAGAACTGAGACGCATTTTGACAATTACAGAGGATGGGCAGGGGCTA
OY  1681 GATRATIC CORCEGAGGAGCAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGG
2019 1621 2079
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Qy 1381 AATTAAGGAGGATTACAAGTGGGAATTTGAAATCCTGTGGTGAGCTGTT
1321 1779

	Query Match 100.0%; Score 3052; DB 24; Length 35935; Best Local Similarity 100.0%; Pred. No. 0; Matches 3052; Conservative 0: Mismatches 0: Indels 0: Gang 0:	LENGTH: 35935 TYPE: DNA ORGANISM: Adenovirus type 5 US-10-433-681-1	PRIOR FILING DATE: 2001-07-13  NUMBER OF SEQ ID NOS: 47  SOFTWARE: Patentin Ver. 2.1  SEO ID NO 1	CURRENT FILING DATE: 2003-06-04 PRIOR APPLICATION NUMBER: PCT/GB02/03211 PRIOR FILING DATE: 2002-07-12 PRIOR APPLICATION NUMBER: GB 0117198 2	APPLICANT: FUERER, CHRISTOPHE TITLE OF INVENTION: ANTI-NEOPLASTIC AGENTS FILE REFERENCE: 604-687 CHEBERUT APPLICATION NUMBER: HS/10/433 681	Publication No. (US20040146856A1 GENERAL INFORMATION: APPLICANT: IGGO, RICHARD APPLICANT: IGGO, KPICZTIAN	RESULT 13 US-10-433-681-1 . Semience 1. Application US/10433681	Gy 3001 CTGGCCTGCACCCGCGCTGAGTTTGGCTCTAGCGATGAAGATACAGATTGAG 3052	Oy 2941 ATTAGGAACCAGCCTGTGATGCTGGATGACCGAGGAGCTGAGGCCCGATCACTTGGTG 3000	Qy 2881 GTGCTGAGGTACGATGAGACCCGCACCAGGTGCAGACCCTGCGAGTGTGGCGGTAAACAT 2940	Qy 2821 GAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTTTGACATGACCATGAAGATCTGGAAG 2880	Qy 2761 AGGGGGGTGTTCCTACCTTACCAATGCAATTTGAGTCACACTAAGATATTGCTTTGAGCCC 2820	Qy 2701 GCCTGGCCAGTGTTTGAGCATAACATACTGACCCGCTGTTCCTTGCATTTGGGTAACAGG 2760	Oy 2641 TGCTCGGACGCAACTGTCACCTGCTGAAGACCATTCACGTAGCCAGCC	Qy 2581 GTGATTAAGCATAACATGGTATGTGGCAACTGCGAGGACAGGGCCTCTCAGATGCTGACC 2640	Qy 2521 AGGGTGCGCCACAATGTGGCCTCCGACTGTGGTTGCTTCATGCTAGTGAAAAGCGTGGCT 2580	Qy 2461 TCAATTAAGAAATGCCTCTTTGAAAGGTGTACCTTGGGTATCCTGTCTGAGGGTAACTCC 2520	Qy 2401 CGGGGCTGTGCCTTTTACTGCTGGAAGGGGGTGGTGTGTCGCCCCAAAAGCAGGGCT 2460
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GATCTGGAAG 3338		3279	뫄
GATCTGGAAG 2880	GAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTTTGACATGACCATGAAGATCTGGAAG	2821	Ş
GCTTGAGCCC 3278	AGGGGGTGTTCCTACCTTACCAATGCAATTTGAGTCACACTAAGATATTGCTTGAGCC	3219	밁
GCTTGAGCCC 2820	AGGGGGGTGTTCCTACCTTACCAATGCAATTTGAGTCACACTAAGATATT	2761	Ş
GGGTAACAGG 3218		3159	ర్జ
GGGTAACAGG 2760	GCTTGGCCAGTGTTTGAGCATAACATACTGACCCGGCTGTTCCTTGCATTTGGGTAACAGG	2701	Ş
CTCTCGCAAG 3158		3099	Дb
CTCTCGCAAG 2700	TGCTCGGACGGCAACTGTCACCTGCTGAAGACCATTCACGTAGCCAGCC	2641	Ş
GATGCTGACC 3098		3039	뫄
GATGCTGACC 2640	GTGATTAAGCATAACATGGTATGTGGCAACTGCGAGGACAGGGCCTCTCAGATGCTGACC	2581	γQ
AAGCGTGGCT 3038	AGGGTGCGCCACAATGTGGCCTCCGACTGTGGTTGCTTCATGCTAGTGAAAAACGGTGGCT	2979	ДĎ
AAGCGTGGCT 2580		2521	Ş
GGGTAACTCC 2978	TCAATTAAGAAATGCCTCTTTGAAAGGTGTACCTTGGGTATCCTGTGTGTG	2919	뫄
GGGTAACTCC 2520	TCAATTAAGAAATGCCTCTTTGAAAGGTGTACCTTGGGTATCCTGTCTGA	2461	Ş
AAGCAGGGCT 2918		2859	뫄
AAGCAGGGCT 2460	CGGGGCTGTGCCTTTTACTGCTGCTGGAAGGGGGTGGTGTGTCGCCCCAAAAGCAGGGCT	2401	δ
TGTAAGGGTT 2858		2799	뫄
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TATCCTACAC 2798	TTTACTGGCCCCAATTTTAGCGGTACGGTTTTCCTGGCCAATACCAACCTTATCCTACAC	2739	뫄
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GAATGTAAGG 2738	ATGATAAATATGTGGCCGGGGGTGCTTGGCATGGACGGGGTGGTTATTATGAATGTAAGG	2679	뫄
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Sequence 1, Application US/10612285

Sequence 1, Application US/10612285

Publication No. US20050175589A1

GENERAL INFORMATION:

APPLICANT: IGGO, RICHARD DEREK

APPLICANT: FUERER, CHRISTOPHE

APPLICANT: HOWICSKO, KRISZTIAN GYULA

TITLE OF INVENTION: ANTI-NEOPLASTIC VIRAL AGENTS

FILE REFERENCE: 604-689

CURRENT APPLICATION NUMBER: US/10/612,285

CURRENT FILING DATE: 2003-07-03

PRIOR APPLICATION NUMBER: 10/433,681

PRIOR FILING DATE: 2003-06-04

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PRIOR APPLICATION NUMBER: PCT/GB02/03211
PRIOR FILING DATE: 2002-07-12
PRIOR APPLICATION UMMBER: GB 0117198.2
PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 1
LENGTH: 35935
TYPE: DNA
ORGANISM: Adenovirus type 5
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  AATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGTCTAGAGAATGCAATAGTAG
                                                                CAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGCATGTTTGTCTACAGTAAGT
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APPLICANT: Graddis, Thomas
APPLICANT: Laus, Reiner
APPLICANT: Laus, Reiner
APPLICANT: Diegel, Michael
APPLICANT: Vidovic, Damir
APPLICANT: Vidovic, Damir
TITLE OF INVENTION: Compositions and Methods Employing Alternative
TITLE OF INVENTION: Reading Frame Polypeptides for the Treatment of
TITLE OF INVENTION: Cancer and Infectious Disease
FILE REFERENCE: 11311.1003U
CURRENT FILING DATE: 2004-03-05
CURRENT FILING DATE: 2004-03-05
NUMBER OF SEQ ID NOS: 733
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 732
LENCTH: 35938
TYPE: DNA
ORGANISM: Adeno Virus
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	ATGAAGATACAGATTGAG 3510	ATGAAGATACAGATTGAG 3052	AGGAGCTGAGGCCCGATCACTTGGTG 3458	AGGAGCTGAGGCCCGATCACTTGGTG 3000	GACCCTGCGAGTGTGGCGGTAAACAT 3398	SACCCTGCGAGTGTGGCGGTAAACAT 2940	TTGACATGACCATGAAGATCTGGAAG 3338	

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I43358 Sequence 1	I38383 Sequence 1	I32051 Sequence 1	AX838364 Sequence		AX449148 Sequence		CQ854905 Sequence	AR230727 Sequence	AR102229 Sequence	AR091536 Sequence	AF534906 Human ade	J01917 Adenovirus	AX770200 Sequence	AX084519 Sequence	AR403724 Sequence	AX084516 Sequence	AX084518 Sequence	AX084505 Sequence	AX084517 Sequence	AX084504 Sequence	AR403723 Sequence	M73260 Mastadenovi	AX683770 Sequence	AX451988 Sequence	AR230724 Sequence

ALIGNMENTS

## REFERENCE AUTHORS RESULT 1 AX770195 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM Ś ORIGIN FEATURES Query Match Best Local Similarity 100. Matches 2594; Conservative JOURNAL TITLE CDS source 1 ATCGATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGT 3408 bp Sequence 6 from Patent WO03035883. AX770195 Hochberg,A. and Ayesh,S. Methods and compositions for inducing tumor-specific cytotoxicity Patent: WO 03035883-A 6 01-MAY-2003; Yissum Research and Development Co. of the Hebrew Univ of Jerusale Human adenovirus type 5 Human adenovirus type 5 Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus. AX770195.1 GI:32437735 ELYDLDVTAPEDPNEBAVSQIFPDSVMLAVQEGIDLLTFPPAPGSPEPPHLSRQPEQPEQPALGPVSMPNLVPEVIDLTCHEAGFPSDDEDEEGEEFVLDVYEHPGHGCRSCHYHRRNTGDPDIMCSLCYMRTCGMFVYSPVSEPEPEPEPEPEPARPTRRPKMAPAILRRPTSPVSRECNSSTDSCDSGPSNTPPEIHPVVPLCPIKPVAVRVGGRRQAVECIEDLLNEPGQPLDLSCKRPRP /protein\_id="CAE01147.1" /db\_xref="GI:32437736" /translation="MRHIICHGGVITEEMAASLLDQLIEEVLADNLPPPSHFEPPTLH /mol\_type="unassigned DNA" /db\_xref="taxon:28285" join(44. .598,715. .1029) Location/Qualifiers codon\_start=1 product="Ela" organism="Human adenovirus type 5" . .3408 100.0%; 0 Score 2594; Pred. No. 0; 0; Mismatches DNA 멾 0; 6 Hebrew Univ of Jerusalem Indels Length linear 3408; PAT 02-JUL-2003 0 Gaps 60 0

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1081 TTTTGAGTTTTATAAAGGATAAATGGACCGAAGCACCATCTGAGCGGGGGTACCTGC 1140	AGAAGGTCATCAAGACTTTGGATTTTTCCACACCGGGGCGCGCTGCGGCTGCTGTTGCTT 1	1301 CCCAGGCAAAGTTAGTCTGCAGAATTAAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTT 1360 961 TGAAATCCTGTGGTGAGCTGTTTGATTCTTTGAATCTGGGTCACCAGGCGCTTTTCCAAG 1020	ACTIGCTEGAACAGAGCTCTAACAGTACCTCTTEGTTTTEGAAGGTTTCTEGTGGGGCTCAT  CCCAGGCAAAGTTAGTCTGCAGAATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTT	ACTIGCTGGAACAGAGCTCTAACAGTACCTCTTGGTTTTTGGAGGTTTCTTTTTGGGGCTCAT	TGGTTACATCTGACCTCATGGAGGCTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGCGTA	TGCATGGCGTGTTAAATGGGGCGGCGTTAAAGGGTATATAATGCGCCGTGGGCTAATCT	CGCCTTTGTTTGCTGAATGAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACT 7	ACTTGAGCTGTAAACGCCCCAGGCCATAAGGTGTAAACCTGTGATTGCGTGTGGGTTAA 6		CTGAGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTG 5	21 TGTCTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTC 4	CAAGACCTACCGGCGTCCTAAAATGGGGGCCTGCTATCCTGAGACGCCCGACATCACCTG 4	TITTITAAAAGGTCCTGIGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTG 3	241 GTGTGGTAATTTTTTTAATTTTTAAGTTTTGTGGTTTAAAGAATTTTGTATTGTGA 300	81 GGCATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTG 2	461 GAGGAGTTTGTGTTAGATTATGTGGAGCACCCCGGCACGGTTGCAGGTCTTGTCATTAT 520  121 CACCGGAGGAATACGGGGGACCCAGATATTATGTGTTTCGCTTTTGCTATATGAGGACCTGT 180	61 GAGGAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTAT 1
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                                             TGTCTAGAGAATGCAATAGTAGTAGGATAGCTGTGACTCCGGTCCTTCTAACACACCTC
                                                                                           CAAGACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTG
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/mol type="unassigned DNA"
/mbxref="taxon:32630"
/noce="plasmid STK146"
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PR 14-JAN-2000 JP 2000593765

PR 14-JAN-1999 US 60/115920

PI GLEN ROBERT NEMEROW, DANIEL J VON SEGGERN, PAUL L HALLENBECK, PI SUSAN C STEVENSON, YELENA SKRIPCHENKO

PC C12N15/09, A61X35/76, A61X48/00, A61P35/00, A61P43/00, A61P43/00, PC C12N5/10,

PC C12N5/10,

PC C12N7/00, C12Q1/68, G01N33/53, G01N33/56, C12N15/00, C12N5/00 CC Description of Artificial Sequence: plasmid FH Key

FT source 1...7607

FT source 1...7607
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(bases 1 to 7607)

Nemerow.G.R., Seggern,D.J.V., Hallenbeck,P.L.,
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/mol_type="genomic DNA"
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Adenovirus vector, packaging cell line, composition and method for production and use
patent: JP 2002534130-A 12 15-OCT-2002;
NOVARTIS AG, THE SCRIPPS RESEARCH INSTITUTE
OS Artificial Sequence
PN JP 2002534130-A/12
PD 15-OCT-2002
PF 14-JAN-2000 JP 2000593765
PF 14-JAN-2000 JP 2000593765
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PI GLEN ROBERT MEMBEROW, DANIEL J VON SEGGERN, PAUL L HALLENBECK, PI SUSAN C STEVENSON, YELENA SKRIPCHENKO
C C12N15/09,A61K35/76,A61K48/00,A61P35/00,A61P43/00, PC C12N15/09,A61K35/76,A61K48/00,A61P35/00,A61P43/00,A61P43/00, PC C12N15/09,C1201/68,G01N33/53,G01N33/566,C12N15/00,C12N5/00 CC DESCRIPTION OF Artificial Sequence: plasmid FH Key Location/Qualifiers
FT Source /organism='Artificial Sequence'.
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1561 CATAGAGCAGCTGACCACTTACTGGCTGCAGCCAGGGGATGATTTTGAGGAGGCTATTAG 1620	TTTTCAACAGATCAAGGATAATTGCGCTAATGAGCTTGATCTGCTGGCGCAGAAGTATTC	1441 AGAGGAGGCTAAGGATCTTAGCTTTAAGCTTAATGACCAGACACCGTCCTGAGTGTATTAC 1500	TACAGAGGATGGGCAGGGGCTAAAGGGGGTAAAGAGGGAGCGGGGGGCTTGTGAGGCTAC	GGGAATGAATGTTGTACAGGTGGCTGAACTGTATCCAGAACTGAGACGCATTTTGACAAT	AAGCCAGGCGGCGGCAGGAGGAGCAGAGCCGAAACCCGAGAGCCGGCTGGACCCTC 1	1 TGTTGTCTTCCGTCCGCCGGCGATAATACCGACGAGGAGGAGCAGCAGCAGCAGGAGGAGG	TGGATTTTCTGGCCATGCATCTGTGGAGAGCGGTTGTGAGACACAAGAATCGCCTGCTAC	TTTGAGTTTTATAAAGGATAAATGGAGCGAAGAAACCCATCTGAGCGGGGGGTACCTGC	AGAAGGTCATCAAGACTTTGGATTTTTCCACACCGGGGCGCGCTGCGGCTGCTGTTTGCTT	TGAAATCCTGTGGTGAGCTGTTTGATTCTTTGAATCTGGGTCACCAGGCGCTTTTCCAAG	CCAGGCAAAGTTAGTCTGCAGAATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTT	ACTTGCTGGAACAGAGCTCTAACAGTACCTCTTGGTTTTTGGAGGTTTCTGTGGGGCTCAT	TGGTTACATCTGACCTCATGGAGGCTTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGCGTA	TGCATGGCGTGTTAAATGGGGGGGGGGTTAAAGGGTATATAATGGGCCGTGGGCTAATCT 	GCCTTTGTTTGCTGAATGAGTTGAATGTTAAGTTTAATAAAGGGTGAGATAATGTTTAACT	ACTIGAGCIGIAAACGCCCCAGGCCATAAGGIGIAAACCIGIGATIGCGIGIGIGIGIAAACGIGIGAAACCIGIGAAACCIGIGAAACGIGIGIGI	GGCGTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGGCCTGGGCAACCTTTTGG	2305 CTGAGATACACCCGGTGGTCCCCCGCTGTGAGACCTGGTGAGAGTTGGTG 2364
RESULT 6 AX356041	Qy 2581 AGATACAGATTGAG 2594	QY 2521 GCTGAGGCCCGATCACTTGGTGCTGGACCCGCGCTGAGTTTGGCTCTAGCGATGA 2580	Qy 2461 CTGCGAGTGTGGCGGTAAACATATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGA 2520	QY 2401 CATGACCATGAAGATCTGGAAGGTGCTGAGGTACGATGAGACCCGCACCAGGTGCAGACC 2460	QY 2341 CACTAAGATATTGCTTGAGCCCGAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTTTGA 2400	Qy 2281 TTCCTTGCATTTGGGTAACAGGAGGGGGGGTGTTCCTACCTTACCAATGCAATTTGAGTCA 2340	Qy 2221 CGTAGCCAGCCACTCTCGCAAGGCCTGGCCAGTGTTTGAGCATAACATACTGACCCGCTG 2280	Qy 2161 CAGGGCCTCTCAGATGCTGACCTGCTCGACGGCAACTGTCACCTGCTGAAGACCATTCA 2220	Qy 2101 CATGCTAGTGAAAAGCGTGGCTGTGATTAAGCATAACATGGTATGTGGCAACTGCGAGGA 2160			OY 1921 AGCCTGGACCGATGTAAGGGTTCGGGGCTGTGCCTTTTACTGCTGCTGGAAGGGGGTGGT 1980	OY 1861 CAATACCAACCTTATCCTACACGGTGTAAGCTTCTATGGGTTTAACAATACCTGTGTGGA 1920	QY 1801 GGTGGTTATTATGAATGTAAGGTTTACTGGCCCCAATTTTAGCGGTACGGTTTTCCTGGC 1860	Qy 1741 TAGGGTGGCCTTTAGATGTAGCATGATAAATATGTGGCCGGGGGTGCTTGGCATGGACGG 1800	Qy 1681 TATCAGGAATTGTTGCTACATTTCTGGGAACGGGGCCGAGGTGGAGATAGAT	OY 1621 GGTATATGCAAAGGTGGCACTTAGGCCAGATTGCAAGTACAAGATCAGCAAACTTGTAAA 1680 	Db 3385 CATAGAGCAGCTGACCACTTACTGGCTGCAGCCAGGGGATGATTTTGAGGAGGCTATTAG 3444

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661 CGCCTTTGTTTGCTGAATGAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACT 720	601 ACTTGAGCTGTAAACGCCCCAGGCCATAAGGTGTAAACCTGTGATTGCGTGTGGGTTAA 660	541 GGCGTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGG 600	481 CTGAGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTG 540	421 TGTCTAGAGAATGCAATAGTAGGATAGCTGTGACTCCCGGTCCTTCTAACACACCTC 480	361 CAAGACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCGACATCACCTG 420		241 GTGTGGTAATTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGA 300	181 GGCATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGGTGG	121 CACCGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGT 180	61 GAGGAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTAT 120	1 ATCGATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGACGAGATGAAGAGGGT 60	Query Match 100.0%; Score 2594; DB 6; Length 11152; Best Local Similarity 100.0%; Pred. No. 0; Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/mol_type="unassigned DNA" /db_xref="taxon:32630" /note="plasmid"	(G	ors for ocular transduction and use thereont: WO 0183729-A 12 08-NOV-2001; rt18 AG (CH); The Scripps Research Instit R. (US); Von Seggern, Daniel J. (US); F			AX356041 11152 bp DNA linear PAT 06-FEB-2002
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1741 TAGGGTGGCCTTTAGATGTAGCATGATAAATATGTGGCCGGGGGTGCTTGGCATGGACGG 1800		1621 GGTATATGCAAAGGTGCACTTAGGCCAGATTGCAAGTACAAGATCAGCAAACTTGTAAA 1680 	CATAGA9CAGCTGACCACTTACTGGCTGCAGCCAGGGATGATTTTGAGGAGGCTATTAG	TTTTCAACAGATCAAGGATAATTGCGCTAATGAGCTTGATCTGCTGGCGCAGAAGTATTC	1441 AGAGGAGCTAGGAATCTAGCTTTAGCTTAATGACCAGACACCGTCCTGAGTGTATTAC 1500	5 12	1321 GGGAATGAATGTTGTACAGGTGGCTGAACTGTATCCAGAACTGAGACGCATTTTGACAAT 1380 	1261 AAGCCAGGCGGCAGGAGCAGAAGCCCATGGAACCCGAGAGCCGGCCTGGACCCTC 1320	01 TGTTGTCTTCCGTCCGCCCGGCGATAATACCGACGAGGAGGAGCAGCAGCAGCAGCAGGAGGAGGAGCAGC	41 65	81 05	1021 AGAAGGTCATCAAGACTTTGGATTTTTCCACACCGGGCGCGCTGCCGCTGCTGCTTGCT	961 TGAAATCCTGTGGTGAGCTGTTTGATTCTTTGAATCTGGGTCACCAGGCGCTTTTCCAAG 1020	901 CCCAGGCAAAGTTAGTCTGCAGAATTAAGGAGGATTACAAGTGGAATTTGAAGAGCTTT 960 	1 ACTTGCTGGAACAGAGCTCTAACAGTACCTCTTGGTTTTTGGAGGTTTCTGTGGGGCTCAT	781 TGGTTACATCIGACCICATGGAGGCTIGGGAGIGTTTGGAAGATTTTTCIGCTGIGGGTA 840	721 TGCATGGCGTGTTAAATGGGGCGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCT 780	CGCCTTTGTTTGCTGAATGAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACT

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RESULT 7
BD021940
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Packaging cell systems for high-capacity adenoviral BD021940
BD021940 GI:22563163
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JP 2001505047-A/12.
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Memerow,G.R. and Seggern,D.J.V.
Packaging cell systems for use in
high-capacity adenoviral vectors
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NOVARTIS AG, THE SCRIPPS RESEARCH INSTITUTE
PN JP 2001505047-A/12
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PF 24-SEP-1997 JP 1998515273
PF 24-SEP-1996 US 08/719806
PR 25-SEP-1996 US 08/719806
PR 25-SEP-1996 US 08/719806
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PR 25-SEP-1996 US 08/719806
PC C12NS/10,C07K14/075,C12N15/09//A61K31/711,A61K35/76,A61K48/00,PC C12N5/00,C12N15/00
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1981 GIRTGGCCCCANANGCNGGGTTCCATTNAGANATGCCTCTTGANAGGTTTACCTTTGGG 2040 3805 TRICCTGTCTGAGGTAACTCCAGGTTCCATTNAGAATGCCTCCTTGANAGGTTTACCTTTGGG 3864 3815 TATCCTGTCTGAGGTTAACTCCAGGTTCGCCCACATTTGGCACTTGGTTGCTT 210 3815 TATCCTGTCTGAGGTTAACTCCCAGGTTCGCCACATTTGGCACTTGGTTGCTT 3924 2101 CATGCTAGTGAAAAGCGTGGCTGTGTTATACACATTACACTTGGTTGCTTTGGTTGCTT 3924 2111 CATGCTAGTGAAAAGCGTGGCTGTGTTATACACATTACACTTGGTCTCCGACTGCTGCAGGAGA 216 2121 CATGCTAGTGAAAAGCGTGGCTGGTCTGATTAACCATTACACTTGTGGCACTTGCGACGAGGA 394 2121 CATGCTAGTAAAAGCGTGGCCTGCTCGGACGGCACTTGTGGCACTTCTGAGACCCCTTCTAAAAGCGTGGCCACTTGTGGGCACTTGTGGCACTTGTGGCACTTGTGGCACTTGTGGCACTTGTGGGCACTTTGAGTCAATGCCTTCTAAAAGCCTTGCCAATGCTTCTACCTTACACATTACATTACTTAGGTCAATTACACAATGCATTACACATTACACATTACATTACTTGGGTCAATTACACAATGCATTACACATTACACATTACACTTGAGTCAATTACTTGGGTAACAATACTTGGGTAACAATACTTCGAAAGGCCTGGCCAGTGTTTCAACAATTACTGAGTCCAATGCAATTACTTGGGTCAATTACACAATTACTTGGGTAACAACATTACACAATGCAATTACTTGGGTAACAACATTACACAATGCAATTACACAATACTTTCCTTCAAGCCCCAAAGAGGGGGGTTTCCTAACCAATGCAATTACAACATTTTTGGTTAACAATATTTCCTTGAAGCCCAAAGAGGGGGGTTTCCTAACCATTACAAATACTTGGTTACAAAAAATATTACATAACAATATTTAGAAAACATTTCGAAACAATATTACAAAAAATATTAGAAAAAATATTAGAAAAAAATATTAAGAAAAAA	625 GGTGGTTATTATGAATGTAAGGTTTACTGGCCCCAAȚTTTAGCGGTACGGTTTTCCTGGC  861 CAATACCAACCTTATCCTACACGGTGTAAGCTTCTATGGGTTTAACAATACCTGTGTGTG

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Mast,J. and Van Ormondt,H.
The nucleotide sequence of the transforming HindIII-G fragment adenovirus type 5 DNA. The region between map positions 4.5 (Hp site) and 8.0 (HindIII site)
Gene 6 (1), 75-90 (1979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Broker,T.R.
Appendix d: nucleotide sequences, transcription and translation
Analyses, and restriction endonuclease cleavage maps of group-c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thimmappaya, B., Jones, N. and Shenk, T. A mutation which alters initiation of transcription by RNA polymerase III on the Ad5 chromosome Cell 18 (4), 947-954 (1979)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 1574)
Van Ormondt,H., Maat,J., De Waard,A. and Van der
The nucleotide sequence of the transforming HpaI-
adenovirus type 5 DNA
Gene 4 (4), 309-328 (1978)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maat, J., van Beveren, C.P. and van Ormondt, H. The nucleotide sequence of adenovirus type 5 early region E1: the region between map positions 8.0 (HindIII site) and 11.8 (SmaI
                Bos,J.L., Polder,L.J., Bernards,R., Schrier,P.I., van den Elsen,P.J., van der Eb,A.J. and van Ormondt,H. The 2.2 kb Elb mRNA of human Adl2 and Ad5 codes for two two antigens starting at different AUG triplets Cell 27 (1 Pt 2), 121-131 (1981)
                                                                                                                                                                   10 (bases 10555 to 10733)

Fowlkes,D.M. and Shenk,T.

Transcriptional control regions of the adenovirus VAI RNA gene CEC1 22 (2 Pt 2), 405-413 (1980)
                                                                                                                                                                                                                                                                                       van Ormondt, H., Maat, J. and van The nucleotide sequence of the adenovirus type 5 DNA Gene 11 (3-4), 299-309 (1980)
                                                                                                                                                                                                                                                                                                                                                                                                                          Perricaudet,M., Le Moullec,J.M. and Pettersson,U. Predicted structure of two adenovirus tumor antigens Proc. Natl. Acad. Sci. U.S.A. 77 (7), 3778-3782 (198
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d Spring Harbor Laboratory (1980)
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transforming HpaI-E fragment
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van Beveren, C.P., Maat, J., Dekker, B.M. and van Ormondt, H.

The nucleotide sequence of the gene for protein IVa2 and of
leader segment of the major late mRNAs of adenovirus type 5

Gene 16 (1-3), 179-189 (1981)
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Nagata, K., Guggenheimer, R.A. and Hurwitz, J.
Specific binding of a cellular DNA replication protein to origin of replication of adenovirus DNA
Proc. Natl. Acad. Sci. U.S.A. 80 (20), 6177-6181 (1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hearing, P. and Shenk, T.

Hearing, P. and Shenk, T.

Functional analysis of the nucleotide site for adenovirus type 5 region EIA J. Mol. Biol. 167 (4), 809-822 (1983)
                                                        the sequence represents the early mrna transcripts ela and elb and the intermediate mrna transcript ix, all of which are transcribed trightwardly off the r-strand; the iva2 and e2b mrnas which are transcribed leftwardly off the 1-strand ((indicated by '(c)' and 'comp strand' below)); and the 5' end of the 28 kb major late mrna. the cap sites and possible promoter sequences for these are summarized in the following table:
                                                                                                                                                                                                                                        This sequence corresponds to bases I to 11560 of <ad2>, which serve as some basis for the annotation of sites the differences between <ad2> and <ad5> are too many to report herein, however a printout of those is available upon request from genbank the map coordinates in the sites presume 360 bases per map unit. although there are approximately 115 sequence differences between the two strains over this region, no site difference exceeds 0.02% by this
                                                                                                                                                                                                                                                                                                                                                                                                      Here Adeno virus sequences are always given in 5' to 3' direction and the sequence of the 1-strand is displayed irrespective of the direction the viral transcription takes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The nucleotide sequence of fragment HindIII-C type 5 DNA (map positions 17.1-31.7) Gene 27 (1), 115-120 (1984)
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Local :
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tatataa at bases 3551-3557 [6] iva2

tacaaa at bases 5979-5974 on the comp strand [10]

major

6049

with ad2, not all the transcripts from this region have been characterized at the sequence level, the nine proteins given in features table below are not the only possible gene products (see the main adenovirus 2 entry).

large amounts of small rnas are produced from the val and vaii genes late in development for unknown reasons. [5] and [6] demonstrate that val gene activity influences vali expression; that the 5' flank affects the start site of the rna but that an intragenic promoter (bases 10636 to 10690 below) determines whether the rna is actually produced; and that there is striking similarity between this rna and trna.

11570

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TGTCTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTC
                                                                                                   CAAGACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTG
                                                                                                                                                                                                                                                                                     GTGTGGTAATTTTTTTTTAATTTTTTACAGTTTTGTGGTTTTAAAGAATTTTTGTATTGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Join (499. 1112,1129. 1632)

/note="mRNA 1 (part 1)"

Join (499. 974,1229. 1632)

/note="mRNA 2 (part 1)"

Join (50. 1112,1229. 1545)

/note="unnamed protein product; Ela pr

(32k, regulation and transformation)"

/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="CAB40663.1"
/db_xref="GI:4584382"
/db_xref="GI:458438
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499. .1632
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                                                                                                                  AGAGGAGGCTAGGAATCTAGCTTTTAGCTTAATGACCAGACACCGTCCTGAGTGTATTAC
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PR 14-JAN-1999 US 60/115920

PI GLEN ROBERT NEMEROW, DANIEL J VON SEGGERN, PAUL L HALLENBECK, PI SUSAN C STEVENSON, YELENA SKRIPCHENKO

PC C12N15/09, A61K35/76, A61K48/00, A61P35/00, A61P43/00, A61P43/00, C12N1/00, C1201/68, G01N33/53, G01N33/566, C12N15/00, C12N5/00, C2 Description of Artificial Sequence: plasmid FH Key Location/Qualifiers

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	481 CTGAGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTG 540	<b>Qу</b> Db 2
3325 TTTTCAACAGATCAAGGATAATTGCGCTAATGAGCTTGATCTGCTGGCGCAGAAGTATTC 3384 1561 CATAGAGCAGCTGACCACTTACTGGCTGCAGCCAGGGGATGATTTTGAGGAGGCTATTAG 1620	5 P	Qy 42 Db 224
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1441 AGAGGAGGCTAGGAATCTAGCTTTTAGCTTAATGACCAGACACCGTCCTGAGTGTATTAC 1500	5 TITTITIAAAAGGICCTGIGTCTGAAACCTGAGCCCTGAGCCCAGCCAGCCAGAACCGGAGCCTG 2184 1 CAAGACCTACCCGCCGCCGTCCTAAAATGGCGCCCTGCTATCCTGAGACGCCCGACATCACCTG 420	Db 212 Qy 36
1381 TACAGAGGATGGGCAGGGGCTAAAGGGGGGTAAAAGAGGGAGCGGGGGGGCTTGTGAGGCTAC 3264 3205 TACAGAGGGATGGGCAGGGGCTAAAGGGGGGTAAAAGAGGGAGCGGGGGGCTTGTGAGGCTAC 3264	1 TTTTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTG	
3145 GGGAATGAAGTTGTACAGGTGGCTGAACTGTATCCAGAACTGAGCGCATTTTGACAAT 3204	1 GTGTGGTAATTTTTTTTTTTTTTTTTACAGTTTTTGTGGTTTTAAAGAATTTTGTATTGTGA 300	Qy 24 Db 206
	181 GGCATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTG 240	Qy :
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1201 TGTTGTTCTTCCGCCCCGGCGATAATACCGACGGAGGAGCAGCAGCAGCAGCAGCAGGAGG 1260	ANGILI GIGITAGAN TALGIGGANGKAK-C-CGGGGGANGGGIGGANGGGANGGANGGANGATAT 1977	Qγ :
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1021 AGAAGGTCATCAAGACTTTGGATTTTTCCACACCGGGGCGCGCTGCGGGCTGCTGTTGCTT 1080		ORIGIN
961 TGAAATCCTGTGGTGAGCTGTTTGATTCTTTGAATCTGGGTCACCAGGCGCTTTTCCAAG 1020 	/OLIGATIANNE PARTICLE CONSTRUCT /MD_type="unassigned DNA" /db_xref="texxon:32630" /note="plasmid" Db	
	Location/Qualifiers	FEATURES source
	Novartis AG (CH); The Scripps Research Institute (US); Nemerow, Glen R. (US); Von Seggern, Daniel J. (US); Friedlander, Marty OV	
841 ACTTGCTGGAACAGAGCTCTAACAGTACCTCTTGGTTTTGGAGGTTTTCTGTGGGGCTCAT 900	R., von Seggern,D.J. and Friedlander,M. or ocular transduction and use thereof for genetic therapy 0183729-A 15 08-NOV-2001;	AUTHORS TITLE JOURNAL
781 TGGTTACATCTGACCTCATGGAGGCTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGCGTA 840	synthetic construct Synthetic construct Oy other sequences; artificial sequences. Db	SOURCE ORGANISM REFERENCE
721 TGCATGGCGTGTTAAATGGGGCGGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCT 780	. GI:18620606	ACCESSION VERSION KEYWORDS
661 CGCCTTTGCTGAATGAGTTGATGTAAGTTTAATAAGGGTGAGATAATGTTTAACT 720 	14455 bp	RESULT 10 AX356044 LOCUS
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Memerow,G.R. and Seggern,D.J.V.

Packaging cell systems for use in promotion o high-capacity adenoviral vectors

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Strandedness: Double;
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741 TAGGGTGGCCTTTAGATGTAGCATGATAAATATGTGGCCGGGGGGTGCTTGGCATGGACGG 18	1681 TATCAGGAATTGTTGCTACATTTCTGGGAACGGGGCCGAGGTGGAGATAGAT	1621 GGTATATGCAAAGGTGGCACTTAGGCCAGATTGCAAGTACAAGATCAGCAAACTTGTAAA 1680 	1561 CATAGAGCAGCTGACCACTTACTGGCTGCAGCCAGGGGATGATTTTGAGGAGGCTATTAG 1620	1501 TTTTCAACAGATCAAGGATAATTGCGCTAATGAGCTTGATCTGCCGGCGCAGAAGTATTC 1560 	1441 AGAGGAGGCTAGGAATCTAGCTTTTAGCTTAATGACCAGACACCGTCCTGAGTGTATTAC 1500	1381 TACAGAGGATGGGCAGGGGCTAAAGGGGGTAAAGAGGGAGCGGGGGGCTTGTGAGGCTAC 1440 	1321 GGGAATGAATGTTGTACAGGTGGCTGAACTGTATCCAGAACTGAGACGCATTTTGACAAT 1380 	1261 AAGCCAGGCGGCGGCAGGAGCAGAGCCCATGGAACCCGAGAGCCGGCCTGGACCCTC 1320	1201 TGTTGTCTTCCGTCCGCCCGGCGATAATACCGACGAGGAGCAGCAGCAGCAGCAGCAGGAGGAGGAGG	1141 TGGATTTTCTGGCCATGCATCTGTGGAGAGGGGTTGTGAGACACAAGAATCGCCTGCTAC 1200	1081 TTTTGAGTTTTATAAAGGATAAATGGAGCGAAGAAAAACCCATCTGAGCGGGGGGGTACCTGC 1140 	1021 AGAAGGTCATCAAGACTTTGGATTTTTCCACACCGGGGCGCTGCGGCTGCTGTTGCTT 1080	961 TGAAATCCTGTGGTGAGCTGTTTGATTCTTTGAATCTGGGTCACCAGGCGCTTTTCCAAG 1020 	901 CCCAGGCAAAGTTAGTCTGCAGAATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTT 960 	841 ACTTGCTGGAACAGAGCTCTAACAGTACCTCTTGGTTTTTGGAGGTTTCTGTGGGGCTCAT 900	781 TGGTTACATCTGACCTCATGGAGGCTTGGGAGTTTTGGAAGATTTTTCTGCTGTGCGTA 840		1 2
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AUTHORS TITLE JOURNAL	ORGANIS	ACCESSION VERSION KEYWORDS	RESULT 12 CQ854906 LOCUS DEFINITION	Db	OV Db	Q Db	Q D	OV Db	Qy Db	Q B	S B :	δ B :	S B :	OV D		Q B	Db Qy	Db Qy
S Hu,F. and Wu,B. Therapy for primary and metastatic cancers D patent: WO 2004066947-A 3 12-AUG-2004;										045	985 221		865	805	3745 AGCCTGGACCGATGTAAGGGTTCGGGGCTGTGCCTTTTACTGCTGCTGGAAGGGGTGGT 3804 1981 GTGTCGCCCCAAAAGCAGGGCTTCAATTAAGAAATGCCTCTTTGAAAAGGTGTACCTTGGG 2040	3685 CAATACCAACCTTATCCTAACGGTGTAAGCTTCTATGGGTTTAACAATACCTGTGTGGA 3744 1921 AGCCTGGACCGATGTAAGGGTTCGGGGCTGTGCCTTTTACTGCTGTGAAGGGGGTGGT 1980	3625 GGTGGTTATTATGAATGTAAGGTTTACTGGCCCCAATTTTAGCGGTACGGTTTTCCCTGGC 3684 1861 CAATAACCTAACCTTACACGTGTAAAGCTTCTATGGGTTTAACAATACCTGTGGGA 1920	3565 TAGGGTGGCCTTTAGATGTAGCATGATAAATATGTGGCCGGGGGTGCTTGGCATGGACGG 3624 1801 GGTGGTTATTATGAATGTAAGGTTTACTGGCCCCAATTTTAGCGGTACGGTTTTCCTGGC 1860

•	901 CCCAGGCAAAGTTAGTCTGCAGAATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTT 960
1921 AGCCTGGACCGATGTAAGGGTTCGGGGCTGTGCCTTTTACTGCTGCTGGAAGGGGGTGGT 1980	OY 841 ACTTGCTGGAACAGAGCTCTAACAGTACCTCTTGGTTTTGGAGGTTTCTGTGGGGGCTCAT 900
	OY 781 TGGTTACATCTGACCTCATGGAGGCTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGGGTA 840
1801 GJIGGTIATTAIGAATGIAAGGTTIACTGGCCCAATTTTAGCGGTACGGTTTTCCTGGC	QY 721 TGCÄTGGCGTGTTAAATGGGGCGGGGCTTAAAGGGTATATAATGGGCCGTGGGCTAATCT 780
1741 TAGGGTGGCCTTTAGATGTAGCATGATAAATATGTGGCCGGGGGTGCTTGGCATGGACGG	OY 661 CGCCTTTGTTTGCTGAATGAGTTGAATGAAGGTTTAAAAGGGTGAGATAATGTTTAACT 720
	Qy       601 ACTTGAGCTGTAAACGCCCCAGGCCATAAGGTGTAAACCTGTGATTGCGTGTGTAA 660       Qy
1621 2537	OY 541 GGCGTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGG 600
	OY 481 CTGAGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTG 540
1501 TITICAACAGATCAAGAATTATTGCGCTAATGAGCTTGATCTGCTGGCGCAGAAGTATTC 	Qy         421 TGTCTAGAGAATGGAATAGTAGGAGAGGGTGTGTGTGAGGTCCTTCTAACACACCTC 480         Qy           111111111111111111111111111111111111
1411 AGAGGAGGCTAGGAATCTAGCTTATGACCAGACACCGTCCTGACTGA	QY 361 CAAGACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTG 420 Db 1277 CAAGACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTG 1336
1381 TACAGAGGATGAGCAGGCTAAAGGGGGTAAAGGAGGAGCCGGGGGGCTTGTGAGGCCTAC	Qy         301         TITITITAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTG         360           Db         1217         TITITITIAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTG         1276
	OY 241 GIGIGGIAATITITITITAATITITIACAGTITITGIGGTTIAAAGAATITITGIATIGA 300
1261 AAGCCNGGCGGCGGCGGCAGAGCCCATGGAACCCGAGAGCCGGCCTGGACCCTC	QY 181 GGCATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGTGATAGAGTGGTGGTTTG 240
1201 TGTTGTTTCCGTCCGGCCGGCGATAATACCGACGGAGGAGCAGCACCAGCAGCAGCAGCAGCAGCAG	Oy         121 CACCGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTTGCTATATGAGGACCTGT 180         Oy         OY
1141 TGATTTTCTGGCCATGCATCTGTGGAGAGCGTTGTGAGACACAGAATCGCCTGCTAC	OY 61 GAGGAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTAT 120
1081 TTTTGAGTTTTATAAAGGATAAATGGAGCGAAGAAACCCATCTGAGCGGGGGGTACCTGC   TTTTGAGTTTTATAAAGGATAAATGGAGCGAAGAAACCCATCTGAGCGGGGGGTACCTGC 1997 TTTTGAGTTTTATAAAGGATAAATGGAGCGAAGAAACCCATCTGAGCGGGGGTACCTGC	QY 1 ATGATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGT 60
1021 1937	Query Match 100.0%; Score 2594; DB 6; Length 32802; Best Local Similarity 100.0%; Pred. No. 0; Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 961 TGAAATCCTGTGGTGAGCTGTTTGATTCTTTGAATCTGGGTCACCAGGCGCTTTTCCAAG 1020	/organism="unidentified adenovirus" /mol_type="unassigned DNA" /db_xref="taxon:10535"
DD 1817 CCCAGGCAAAGTTAGTCTGCAGAATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTT 1876	Shanghai Sunway Biotech Co Ltd (CN) Location/Qualifiers

1141 TGGATTTTCTGGCCATGCATCTGTGGAGAGCGGTTGTGAGACACAAGAATCGCCTGCTAC 1200		917 ATCGATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATG	, pb
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1021 AGAAGGTCATCAAGACTITGGATTTTTCCACACCGGGGGGGGGG	ρ <sub>b</sub>		ORIGIN Query M
961 TGAAATCCTGTGGTGAGCTGTTTGATTCTTTGAATCTGGGTCACCAGGCGCTTTTCCAAG 1020 	Qy Db	O	Bourc
	Qy Db	Replication- Patent: WO ( Saint Louis	TITLE JOURNAL FEATURES
841 ACTTGCTGGAACAGAGCTCTAACAGTACCTCTTGGTTTTTGGAGGTTTCTGTGGGGCTCAT 900	tadenovirus. Qy	1 Human adenovirus C Viruses; dsDNA viruses, no RNA sta 1 Wold, W.S., Toth, K., Doronin, K. and	ORGANISM REFERENCE AUTHORS
781 TGGTTACATCTGACCTCATGGAGGCTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGCGTA 840	dd Qy	AX084506.1 GI:13	ACCESSION VERSION KEYWORDS SOURCE
721 TGCATGGCGTGTTAAATGGGGCGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCT 780 	28-1		RESULT 13 AX084506 LOCUS DEFINITION
661 CGCCTTTGCTGATGAGTTGATGTAAGTTTAATAAAGGTGAGATAATGTTTAACT /20 		3497 AGATACAGATTGAG 3510	рь
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481 CTGAGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTG 540	GCAGACC 3376 Qy	17	
TGTCTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCCTC	2460	401	ОБ ОУ 2
1277 CAAGACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTG 1336	INTERNATION   DE   DE     CONTROL     CONTROL   CONTRO	ω 4 1	
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301 TITITITAAAAGGICCIGIGICIGAACCIGAGCCIGAGCCAGCCAGAACCGGAGCCIG 360	υc	137	
241 GIGIGGIAATTITITITITAATITITAAAGATTITGTGGITIAAAGAATTITGTATTCIGA 300 	CATTCA 3136 Qy	077	
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61 GAGGAGTTTGTGTTAGATTATGTGGAGGCACCCCGGGGCACGGTTGCAGGTCTTGTCATTAT 120	CTTGGG 2956 QY	897 GTGTCGCCCCAAAAGCAGGGCTTCAATTAAGAAATGCCTCTTTGAAAGGTGTACCTTGGG	Db 2

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	1981 GTGTCGCCCAAAAGCAGGGCTTCAATTAAGAAATGCCTCTTTGAAAGGTGTACCTTGGG 2040 	28
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Human adenovirus C
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
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                                                                                                CACCGGAGGATACGGGGGACCCAGATATTATGTGTTTCGCTTTGCTATATGAGGACCTGT 180
                                                                                                                                                                                                     GAGGAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTAT 120
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GTGTGGTAATTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTTGTATTGTGA
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                                                                 GAGGAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTAT 1036
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                                                                                                                                                                                                                                                                                                                   /organism="Human adenovirus
/mol_type="unassigned DNA"
/db_xref="taxon:129951"
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### AGCCTGGACCGATGTAAGGGTTCGGGGGCTTTTTACTGCTGTGAAGGGGTTGGA  1981 GTGTCGCCCCAAAAGCAGGGCTTCAATTAAGAAATGCCTCTTTTACTGCTGGAAGGGGGTGGGCT  1981 GTGTCGCCCCCAAAAGCAGGGCTTCAATTAAGAAATGCCTCTTTTAAAGGTTGTACCTTTGGG  2040 [		OY  841 ACTTGCTGGAACAGAGCTCTAACAGTACCTCTTGGTTTTGAAGGTTTCTGTGGGGCTCAT 900  1157 ACTTGCTGGAACAGAGCTCTAACAGTACCTCTTGGTTTTGAAGAGTTTCTGTTGGGGCTCAT 181  OY  901 CCCAGGCAAAGTTAGTCTGCAGAATTAAGAGGATTACAAGTGGAAATTTGAAGAGCTTT 960  1817 CCCAGGCAAAGTTAGTCTGCAGAATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTT 187  OY  961 TGAAATCCTGTGGTGAGCTGTTTGATTCTTTGAATTCAAGTGGGAATTTGAAGAGCTTT 187  OY  961 TGAAATCCTGTGGTGAGCTGTTTGATTCTTTGAATCTGGGTCACCAGGCGCTTTTCCAAG  102 1877 TGAAATCCTGTGGTGAGCTGTTTGATTCTTTGAATCTCGGGTCACCAGGCGCTTTTCCAAG  DD  1037 AGAAGGTCATCAAGACTTTTGAATTTTCCACACCGGGGGCGCTGCCGGTGTGCTTTCCAAG  OY  1041 TTTTGAGTTTTATAAAGGATTAATTCCACACCGGGGGCGCTTGCGGTTGCTTTCTT  108 1111111111111111111111111111111111
	276	OY  301 ITTTTTTAAAAGGTTCCTGTGTCTGAACCTGAGCCCGAGCCCGAGCCCTG Bb 1217 ITTTTTTAAAAGGTTCCTGTGTCTGAACCTGAGCCCGAGCCCGAGCCCGAGCCTG Bb 1217 ITTTTTTAAAAGGTTCCTGTGTCTGAACCTGAGCCCGAGCCCGAGCAACCGGAGCCTG  OY  361 CAAGACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCGACATCACCTG  120  OY  421 TGTCTAGAGAATGCAATAGTAGTAGTAGCTGTAACCAGGTCCTTCTAACACCCTC  1337 TGTCTAGAGAATGCAATAGTAGTAGTAGCTGTGACTCCGGTCCTTCTAACACACCTC  140  Db 1337 TGTCTAGAGAATGCAATAGTAGTAGTAGCTGTGACCCGGTCCTTCTAACACACCTC  151  OY  481 CTGAGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTAGAGTTGGTG  1527 CTGAGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTAGAGTTTGGT  1539 CTGAGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTAGAGTTTGGT  1541 GGCGTCGCCAGGCTGTGGAATGTATCGAGGACTTTGCTTAACCAGCCTTCGGAACCTTTGG  1551 GGCGTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTTAACGAGCCTTGGGCAACCTTTGG  1551 GGCGTCGCCAGGCTGTGGAATGTATCGAGGACTTTAACGAGCCTTGGGCAACCTTTAG  OY  661 ACTTGAGCTGTAAACCCCCCAGGCCATAAGGTGTAAACCTGTGATTACGTGTGTAACT  157 CGCCTTTGTTTGCTGAATGATGTTGATGTAAAGGTTAAAACCTGTGATTAACTTTAACT  OY  661 CGCCTTTGTTTGCTGAATGAGTTGAATGTTTAATAAAGGGTGAGATAATGTTTAACT  OY  721 TGCATGGCGTTAAATGGGGCCCAATGAGTTTAATAAAGGGTGAGATAATGTTTAACT  OY  661 CGCCTTTGTTTGCTGAATGAGTTGAATGTTTAATAAAGGGTGAACATAATGTTTAACT  72  OY  721 TGCATGGCGTGTAAATGGGGCCATAAAGGGTTAAATGGCGCCGTGGGCTAATCT  16  OY  721 TGCATGACGTTTAAATGGGGCCCTTAAAGGGTTAAATGTGCGCCGTGGGCTAATCT  16  OY  721 TGCATGACTTTAAATGGGGCCGGGGCTTAAAGGGTTATAATGCGCCCGTGGGCTAATCT  16  OY  721 TGCATGACTTTAAATGGGGCCGGGGCTTAAAGGGTTATATTATGCGCCCGTGGGCTAATCT  16  OY  721 TGCATGCACTCTAATGGGGCCGGGGCTTAAAGGGTTATATTATTCTTGCTTG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                    CDS
  intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATA_eignal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3377 CTGCGAGTGTGGCGGTAAACATATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGA 3436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (09-JUL-2003) Process Sciences, Canji Inc.,
Schering-Plough Corporation, 3525 John Hopkins Court,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human adenovirus C serotype 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 35934)
Sugarman, B.J., McAllister, D.L. and Hutchins, B.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sugarman, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McAllister, D.L., Lu, F., Thomas, B.K., Hutchins, B.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
1 (bases 1 to 35934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human adenovirus C
Human adenovirus C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AY339865.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AY339865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete Nucleic Acid Sequence of the Adenovirus Type 5 Reference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ioprocessing (2003) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGATACAGATTGAG 2594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTGAGGCCCGATCACTTGGTGCTGGCCTGCACCCGCGCTGAGTTTGGCTCTAGCGATGA 2580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGATACAGATTGAG 3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTGAGGCCCGATCACTTGGTGCTGGCCTGCACCCGCGCTGAGTTTTGGCTCTAGCGATGA 3496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                    /trānslation="mRHIICHGGVITEEMAASLLDQLIEEVLADNLPPPSHFEPPTLH
ELYDLDVTAFEDPNEEAVSQIFPDSVMLAVQEGIDLLTFPPAFGSPEPPHLSRQPEQP
EQRALGPVSMPNLVEBVIDLTCHEAGGPPPSDDEDEEGEBFVLDYVEHGGHGCRSCYH
RRNTGDPDIMCSLCYMRTCGMFVYSPVSEPEPEPEPEPEPARPTRRPKMAPAILRRPT
                        AVECIEDLLNEPGQPLDLSCKRPRP"
                                            ELYDLDVTAPEDPNEEAVSQIFPDSVMLAVQEGIDLLTFPPAPGSPEPPHLSRQPEQP
EQRALGPVSMPNLVPEVIDLTCHEAGFPPSDDEDEEGPVSEPEPEPEPEPEPARFTRR
PKMAPAILKRPTSPVSRECNSSTDSCDSGPSNTPPEIHPVVPLCPIKPVAVRVGGRRQ
                                                                                                                                                                                                                                                                                                                              SPVSRECNSSTDSCDSGPSNTPPEIHPVVPLCPIKPVAVRVGGRRQAVECIEDLLNEP
                                                                                                                                       /product="27 kDa protein"
/protein_id="AAQ19285.1"
/db_xref="GI:33465832"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /_____SbU. .1112,1229. .1545)
/gene="EIA"
                                                                                                                                                                                                                                                         'gene="E1A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="5' inverted terminal repeat"
/rpt_type=inverted
168._.1632
                                                                                                                    translation="MRHIICHGGVITEEMAASLLDQLIEEVLADNLPPPSHFEPPTLH"
                                                                                                                                                                                                                                     note="derived from the E1A
                                                                                                                                                                                                                                                                               oin(560. .974,1229. .1545)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product="32 kDa protein"
protein_id="AAQ19284.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="E1A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mol_type="genomic DNA"
serotype="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Human adenovirus C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="derived from the E1A 13S mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="ElA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:33465830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     xref="taxon:129951"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    xref="GI:33465831"
                                                                                                                                                                                                                                                                                                        SCKRPRP"
                                                                                                                                                                                                               start=1
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                                                                                                                                                                                                                                     12S mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="E1B"
1714.
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1672 .3509
                                                                                                                                                                                                                                                      /translation= metrgrrpaalqhqqpqpqahpgqraarsaplhrdpdyadedpa
pubehdpapegraptayqxrpqpakrgdmldrdaybqvteubrlellgqtiksum
pubehdpapegrapiqellsiggerladivaemmyrdbulabyapllrddggggsly
qlqpvigviygptgcgksqllrnllssqlisptpetvffiapqvdmippselkamemq
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="E1B/pIX"
complement(join(4091. .5427,5706. .5718))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAQ19288.1"
/db xref="GI:33465835"
/db xref="GI:33465835"
/translation="MSTNSFDGSIVSSYLTTRMPPWAGVRQNVMGSSIDGRPVLPANS
TTLTYETVSGTPLETAASAAASAAAATARGIVTDFAFLSPLASSAASRSSARDDKLTA
LLAQLDSITRELNVVSQQLLDLRQQVSALKASSPPNAV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAAAAAGGSQAAAAGAEPMEPESRPGPSGMVVVQVAELYPELRRILTITEDGQGLKG
VKRERGACEATEEARNLAFSLMTRHRPECITFQQIKDNCANELDLLAQKYSIEQLTTY
WLQPGDDFEEAIRVYAKVALRPDCKYKISKLVNIRNCCYISGNGAEVEIDTEDRVAFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /trānslation="meawecledfsavrnlleqssnstswfwrflwgssqaklvcrik
EDYKWEFEELLKSCGELFDSLNLGHQALFQEKVIKTLDFSTPGRAAAAVAFLSFIKDK
WSEETHLSGGYLLDFLAMHLWRAVVRHKNRLLLLSSVRPAIIPTEEQQQQQEEARRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="E1B"
1672. .1678
                                                                                                                                                             TPQHEALQWCYLHPRDGLMPMYLNIQSHLYHVLEKIHRTLNDRDRWSRAYRARKTPK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVRVRGCAFYCCWKGVVCRPKSRASIKKCLFERCTLGILSEGNSRVRHNVASDCGCFM
LVKSVAVIKHMVCGNCEDRASQMLTCSDGNCHLLKTIHVASHSRKAWPVFEHNILTR
                                                                                      /note="compared to Ad2WT of NC_001405; his to gln change"
                                                                                                                                                                                 ICEGNYAPGPDGTIIPQSGTLRPRFVKMAYDDLILEHNYDVSDPRNIFAQAAARGPIA
IIMDECMENLGGHKGVSKFFHAFPSKLHDKFPKCTGYTVLVVLHNMNPRRDMAGNIAN
LKIQSKMHLISPRMHPSQLNRFVNTYTKGLPLAISLLLKDIFRHHAQRSCYDWIIYNT
                                                                                                                                                                                                                                                                                                                                                  /product="E2B IVa2"
/protein_id="AAQ19289.1"
/db_xref="GI:33465836"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRPCECGGKHIRNQPVMLDVTEELRPDHLVLACTRAEFGSSDEDTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="E1B 55K"
/protein_id="AAQ19287.1"
/db_xref="GI:33465834"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="E1B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/product="E1B_19K"
/protein_id="AAQ19286.1"
/db_xref="GI:33465833"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="E1A"
1632
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                   note="compared to GenBank Accession Number M73260"
replace="g"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :SLHLGNRRGVFLPYQCNLSHTKILLEPESMSKVNLNGVFDMTMKIWKVLRYDETRTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMINMWPGVLGMDGVVIMNVRFTGPNFSGTVFLANTNLILHGVSFYGFNNTCVEAWT
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/note="B1A 12S"
                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="E1B/protein IX"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="protein 9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MERRNPSERGVPAGFSGHASVESGCETQESPATVVFRPPGDNTD
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Query Match
Best Local Similarity
Matches 2594; Conserv
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ATCGATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGT 60
                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_statt=1
//codon_statt=1
//codon_statt=1
//protein_statt=1
/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="for E2B IVa2 mRNA" 6018. .6024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEHRLLPYSESRPNPRNEEICWIEMP" complement (5428. .5705)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="E2B 120K DNA polymerase"
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/db_xref="GI:33465837"
                                                                                                                                                                                                          QHSRDNEAFRDALLMI VEPEGRWLLDLINILQSI VVQERSLSLADKVAA INYSMLSIS
KFYARRI YHTTYVPI DKEVKI EGFYMMMALKVLTLSDDLGVYRNER I HKAVSVSRRRE
LSDRELMHSLQRALAGTGSGDREAESYFDAGADLRWAPSRRALEAAGAGPGLAVAPAR
AGNVGGVEEYDEDDEYEPEDGEY"
                                                                                                                                                                                                                                                                                                       /translation="MHPVLROMRPPPOORQEQEQROTCRAFSPPPTASGGATSAVDAA
ADGDYSPPRRAARHYLDIESGSGLARLGAPSPERPHPRVQLKRDYREAYVPRONLFRDR
EGEBEPEMRORKFHAGRELHRIGLINFSKLLFESDFEDDARFIGISPARAHYADADLUTAF
EQTVNQEINFQKSFNNHVRTLVAREEVAIGLMHLWDFVSALEQNPNSKPLMAQLFLIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EILRQAAVNDTEIDSVELSFRFKLTGPVVFTQRRQIQEINRRVVAFASNLRAQHQLLP
ARGADVPLPPLPAGPEPPLPPGARPRHRF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="major late mRNAs TATA
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                                                                                                                                        /replace="c"
                                                                                                                                                              note="compared to GenBank Accession
                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/product="L1 52, 55K"
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/db_xref="GI:33465839"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="compared to Ad2WT of NC_001405;
/replace="a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="putative precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       replace="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="compared to GenBank Accession Number M73260"
replace="q"
                                                                 100.0%;
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                                                                 Score 2594;
Pred. No. 0;
                                              Mismatches.
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TTTTGAGTTTTATAAAGGATAAATGGAGCGAAGAAACCCATCTGAGCGGGGGGTACCTGC
                                                                                                                                                                                                                                                                                             CCCAGGCAAAGTTAGTCTGCAGAATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTT
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                                                                                                    AGAAGGTCATCAAGACTTTGGATTTTTCCACACCGGGGCGCGCTGCGGCTGCTGTTGCTT
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2100 3016	41 TATCCTGTCTGAGGGTAACTCCAGGGTGCGCCACAATGTGGGCCTCCGA
2040 2956	981 GTGTCGCCCCAAAAGCAGGGCTTCAATTAAGAAATGCCTCTTTG 
1980 2896	921 AGĆCTGGACCGATGTAAGGGTTCGGGGCCTGTGCCTTTTACTGCT
1920 2836	861 CAÁTACCAACCTTATCCTACACGGTGTAAGCTTCTATGGGTTTAA 
1860 2776	801 GGTGGTTATTATGAATGTAAGGTTTACTGGCCCCAATTTTAGC 
1800 2716	741 TAGGGTGGCCTTTAGATGTAGCATGATAAATATGTGGCCGGGGGTGCTTGGCATGG 
1740 2656	681 TATCAGGAATTGTTGCTACATTTCTGGGAACGGGGCCGAGGTGGAGA 
1680 2596	621 GGTATATGCAAAGGTGGCACTTAGGCCAGATTGCAAGTACAAGAT 
1620 2536	561 CATAGAGCAGCTGACCACTTACTGGCTGCAGGCGAGGGGATGATTTTGAGGAGGCTF 
1560 2476	501 TTTTCAACAGATCAAGGATAATTGCGCTAATGAGCTTGATCTGATCTGATCTTCAACAGATCAAGGATAATTGCGCTAATGAGCTTGATCTGATCAATGAGCTTGATCAATGAGCTTGATCAATGAGCTTGATCAATGAGCTTGATCATCTGATCTGATCTGATCTGATCTGATCATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCATCTGATCATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCATCTGATCATCTGATCATCTGATCATCTGATCATCTGATCATCTGATCATCTGATCATCTGATCATCTGATCATCTGATCATCTGATCATCTGATCATCTGATCATCTGATCATCTGATCATCTGATCATCTGATCATCATCATCATCATCATCATCATCATCATCATCATCA
1500 2416	441 AGAGGAGGCTAGGAATCTAGCTTTTAGCT
1440 2356	381 TACAGAGGATGGGCAGGGGCTAAAGGGGGGTAAAGI 
1380 2296	21 GGGAATGAATGTTGTACAGGTGGCTGAACTGTAT 
1320 2236	261 AAGCCAGGCGGCGGCGGCAGGAGCAGAGCCCATGGAACCCGJ
1260 2176	201 TGTTGTCTTCCGTCCGCCCGGCGATAATACCGACGGA
1200 2116	141 TGATTTTCTGGCCATCCATCTGTGGAGAGCGGTTGTGAGACACAAGAATCG
2056	997 TTTTGAGTTTTATAAAGGATAAATGGAGCGAAGAAACCCATCTGAGCGGGGGGTACC†G

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Acc85140 Human ade	Aav07261 Adenovira	Adk65745 Human ade	Ads00148 Human ade	Adf60698 Ad6 genom	Acc70007 Nucleotid	Abs69881 Human ade	Aac85025 Adenoviru	Aad27972 Recombina	Aac85022 Adenoviru		Aac85019 Adenoviru	Aac85023 Adenoviru	Aac85018 Adenoviru	Aas15612 Mouse ost	Aad27971 Recombina	Adr41672 Wild type	Aca60761 Human ade	Aca61117 Adenoviru	Aca61116 Adenoviru	Abs69883 Human ade	Abs69882 Human ade	Aac85026 Complete	Aav07258 Adenoviru	Abz82331 Human ade

## ALIGNMENTS

RESULT 1 ACC70006

ACC70006 standard; cDNA; 3408 BP.

29-JUL-2003 (first entry)

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exon
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       Hochberg A,
                                                                    01-MAY-2003.
                                                                                   WO2003035883-A2
                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                     gene; ss.
                                                                                                                                                                                                                                          Cancer; hyperproliferative disorder; viral vector; H19 promoter; carcinoma; sarcoma; adenoma; ganglioblastoma; bladder carcinoma; Ela;
                                                                                                                                                                                                                                                                 Nucleotide sequence of the Ela protein of human adenovirus type
                       (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM
                                     22-OCT-2001; 2001US-00012131
                                                   22-OCT-2002; 2002WO-IL000843
                                                                                                                                        intron
                                                                                                                                                                                                                     Human adenovirus type 5.
     Ayesh S;
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/number= 1
599. .714
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note= "contains an intron"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The specification describes a method of treating cancer or hyperproliferative disorders. The method comprises administering conditionally replicative viral vector, where at least one of conditionally replicative viral vector, where at least one of uncleic acids encoding a product essential for its replication operably linked to an H19 regulatory sequence. The method is untreating cancer or hyperproliferative disorders. The cancer is from many different types, for example, carcinoma, sarcoma, addiganglioblastoma. Preferably, the cancer is bladder carcinoma. The sequence encodes the E1a protein of human adenovirus type 5. If linked to a H19 regulatory sequence, and used to produce vector in the method of the invention
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P-PSDB; ABR55301.
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3-441263/41. ABR55301.	ф	1061 CGCCTTTGTTTGCTGAATGAGTTGAAGTTTAATAAAGGGTGAGATAATGTTTAACT 1120
cancer or hyperproliferative disorder comprises administering a nally replicative viral vector, where the viral nucleic acid a product essential for its replication is operably linked to	р Q	721 TGCATGGCGTGTTAAATGGGGCGGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCT 780
rig 7; 122pp; English.	유 &	781 TGGTTACATCTGACCTCATGGAGGCTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGCGTA 840
ification describes a method of treating cancer or liferative disorders. The method comprises administering a nally replicative viral vector, where at least one of the viral	B 8	ACTTGCTGGAAC
linked to an H19 regulatory sequence. The method is useful for cancer or hyperproliferative disorders. The cancer is selected v different types, for example, carcinoma, sarcoma, adenoma and	Q	CCCAGGCAAAGT
lastoma. Preferably, the cancer is bladuer carcinoma. The present encodes the Ela protein of human adenovirus type 5. It was o a H19 regulatory sequence, and used to produce vectors for use athad of the invention	Q V	TGAAATCCTGTGGTGAGCTGTTTGAATTCTTTGAATCTGGGTCACCAGGCGCTTTTTCCAAG
3408 BP; 767 A; 764 C; 1007 G; 870 T; 0 U; 0 Other;	& B	
100.0%; Score 2594; DB 9; Length 3408; Similarity 100.0%; Pred. No. 0; 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db	AGAAGGTCATCAAGACTTTGGATTTTTCCACACCGCGGGGGGGG
ACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGT	Db Qy	1081 TTTTGACTTTTATAAAGGATAAATGGAGCGAAGAAGCCCATCTGAGCGGGGGGTACCTGC 1140
12	B &	1141 TGGATTTTCTGGCCATGCATCTGTGGAGAGCGCTTGTGAGACACAAGAATCGCCTGCTAC 1200
GAGGACCTGT 18	D	1201 TGTTGTCTTCCGTCCGCCGGCGATAATACCGACGAGGAGCAGCAGCAGCAGCAGCAGGAGG 1260
	D Q	1261 AAGCCAGGCGGCGGCGGCAGGAGCAGAGCCCATGGAACCCGAGAGCCGGCCTGGACCCTC 1320 
GGCATGTTTGTCTACAGTAAGTGAAAATTAIGGGCAGTGATAAAGAATTTTGTATTGTGA 300	р Q	1321 GGGAATGAATGTTGTACAGGTGGCTGAACTGTATCCAGAACTGAGACGCATTTTGACAAT 1380 
	D Qy	1381 TACAGAGGATGGGCTAGAGGGGGTAAAGAGGGAGCGGGGGGTTGTGAGGCTAC 1440
	D Qy	1441 AGAGGAGGCTAGGAATCTAGCTTTAGCTTAATGACCAGACACCGTCCTGAGTGTATTAC 1500 
	dy VQ	1501 TTTTCAACAGATCAAGGATAATTGCGCTAATGAGCTTGATCTGCTGGCGCAGAAGTATTC 1560 
	P &	1561 CATAGAGCAGCTGACCACTTACTGGCTGCAGCCAGGGGATGATTTTGAGGAGGCTATTAG 1620
	dg VQ	1621 GGTATATGCAAAGGTGGCACTTAGGCCAGATTGCAAGTACAAGATCAGCAAACTTGTAAA 1680 
660	Qy Db	1681 TATCAGGAATTGTTGCTACATTTCTGGGAACGGGGCCGAGGTGGAGATAGAT
ACTTGAGCTGTAAACGCCCCAGGCCATAAGGTGTAAACCTGTGATTGCGTGTGTGT	S	1741 TAGGGTGGCCTTTAGATGTAGCATGATAAATATGTGGCCGGGGGTGCTTGGCATGGACGG 1800

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Synthetic
                          Gene therapy; amniocyte; cytostatic; Ad5; ElA modified tropism; tumor; PCR primer; 88.
                                                                                                                                                              AAH20746 standard;
                                                                        Plasmid
                                                                                                     13-AUG-2001
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                                                                                                                                                              DNA; 7090
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                                          E1B
                                          region;
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This invention describes novel permanent amniocyte cell lines (A), containing at least one nucleic soid (I) that causes expression of the gene products (II) of the adenoviral EIA and EIB regions. (A) are used to produce gene therapy vectors, especially adeno, adeno-associated, retro or lenti viral vectors, particularly first- or second generation, large-capacity or deleted adenoviral vectors. (A) are also used to produce adenoviral mutants, optionally with modified tropism. The vectors may express a wide range of therapeutic proteins or antisense RNAs. Adenoviral mutants, unable to express the EIB 55 kDa protein, are useful for treating tumors, they replicate in the cells but not significantly in normal primary cells. (A) can be made efficiently, simply and reproducibly. The products of the invention have cytostatic activity. This sequence represents a PCR primer used in the amplification of Adenovirus Ad5 DNA which is described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                     New permanent amniocyte cell lines, useful for producing viral therapy vectors or mutant adenoviruses, express the adenoviral
                                                                                                                                                                                                                                                                                                                              Example 1; Page 67-72; 72pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kochanek S,
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and

Query Match 100. Best Local Similarity 100. Matches 2594; Conservative Sequence 7090 BP; 1696 A; 1685 C; 1882 G; 1827 T; 0 U; 0 Other; 100.0%; Score 2594; 100.0%; Pred. No. 0; DB 5 Length 7090;

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0; Mismatches

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Best Local Similarity
Matches 2594; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The specification describes a nucleic acid molecule comprising an adenovirus (AV) tripartite leader (TPL) nucleotide with a sequence comprising two different TPL exons or three same or different TPL exons. The nucleic acid is used to produce an adenovirus vector particle, deliver an exogenous gene to a target cell, pseudotype recombinant viral vectors, target an adenovirus vector to a cell, produce a modified adenovirus, deliver a heterologous gene to an animal and produce a gutless adenoviral vector particle. The present sequence represents plasmid GRES-E1-SV40-Hygro, which is used in the course of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid comprising for producing high-capacity gene therapy.
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tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                       Nucleotide
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WPI; 2002-082846/11.

Polynucleotide for making vectors, useful for treating ocular diseases, e.g., retinitis pigmentosa, comprises adenovirus inverter terminal repe retinitis pigmentosa, comprises adenovirus inverter termir nces, packaging signal and photoreceptor-specific promoter.

Example 5; Page 139-141; 149pp; English.

The invention provides an isolated polynucleotide comprising adenovirus CC (AV) inverter terminal repeat sequences (ITRS), AV packaging signal CC operatively linked to ITRS and a photoreceptor-specific promoter. A CC recombinant AV vector (AVV) comprising the polynucleotide is useful for CC targeted delivery of a gene product to the eye (especially to the CC degenerative disease, retinitis pigmentosa, Stargardt's disease, diabetic CC degenerative disease, retinitis pigmentosa, Stargardt's disease, of a mammal CC preferably human. The AAV comprises a fiber protein that specifically or CC generatively binds to receptors that are expressed on cells (preferably photoreceptors in the eye). Preferably, the recombinant virus comprise a CC fiber protein from an adenovirus type D subgroup or is a chimeric protein CC containing a portion of the N-terminus of an adenovirus type 2 or type 5 apoptotic factor, gene encoding a rhodopsin protein, a wild-type stargardt disease gene (STDG1), an anti-cancer agent and a protein that regulates expression of a photoreceptor specific gene product. The viral comprises and packaging signal derived from AAV cubgroup B or C, especially an AV type 2 or type 5. AAV is also useful for targeted gene therapy, where the vector comprises an AV type 37 fiber

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein or its portion, and selectively transduces photoreceptors and delivers a gene product encoded by AAV. The present sequence represents the nucleotide sequence of plasmid GRES-E1-SV40-Hygro
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      GTGTCGCCCCAAAAGCAGGGCTTCAATTAAGAAATGCCTCTTTGAAAAGGTGTACCTTGGG 2040
                                  AGCCTGGACCGATGTAAGGGTTCGGGGCTGTGCCTTTTACTGCTGGAAGGGGGTGGT 1980
                                                               CAATACCAACCTTATCCTACACGGTGTAAGCTTCTATGGGTTTTAACAATACCTGTGTGGA 1920
                                                                                           GGTATATGCAAAGGTGGCACTTAGGCCAGATTGCAAGTACAAGATCAGCAAACTTGTAAA 1680
                                                                                                                                                                                                               TACAGAGGATGGGCAGGGGCTAAAGGGGGTAAAGAGGGAGCGGGGGGCTTGTGAGGCTAC
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                                                                                24-JAN-2002; 2002US-0350388P.
26-JUN-2002; 2002US-0391967P.
                                                                                                                                                                                                                      Rhesus macaque polyoma virus.
Unidentified adenovirus.
                                                                                                                                                                                                                                                               Fibre shaft modification; adenoviral vector; cell entry pathway; penton; CAR; coxsackie adenovirus receptor; heparin sulphate proteoglycan; HSP; gene therapy; fibre knob; ds.
                                                                                                                                                                                                                                                                                                                       DNA sequence of the plasmid GRE5-E1-SV40-Hygro construct
                                                                                                                                                                                                                                                                                                                                                                                                          AAL56864 standard; DNA;
              Kaleko M,
                                                                                                                         24-JAN-2003; 2003WO-US002295.
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              Nemerow GR,
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              Smith
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                Stevenson
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This invention relates to novel fibre shaft modifications in adenoviral convectors. Adenoviral vector-mediated gene therapy aims to transduce a specific targeted tissue or organ, accordingly gene therapy requires the specific targeted to transduce and converted to the desired location in the converted peripheral vein would be targeted to the desired location in the converted without any associated side effects, which would permit lower, less toxic vector doses that are also potentially less immunogenic. The converted invention describes capsid modifications, specifically fibre converted to the parin sulphate proteoglycans (HSP) thus providing detargeted binding to heparin sulphate proteoglycans (HSP) thus providing detargeted converted proteins involved in the cell entry pathway such as the fibre knob, penton or CAR (coxsackie adenovirus receptor) proteins, the vectors become fully detargeted. As such, these fully ablated particles can be used in vivo as base vectors such, these fully ablated adenoviruses with the desired cell specificity. This polymucleotide sequence is the plasmid content of the function of the involved complementation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      producing redirected adenoviruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New modified adenovirus capsid protein, useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-627459/59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 141-143; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a base vector
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Sequence 7607 BP; 1838 A; 1733 C; 2001 G; 2035 T; 0 U; 0 Other; adenoviral E1 function of the invention

Query Match Best Local Similarity

100.0%;

Score 2594; Pred. No. 0;

명 9

Length

á Ś S S 맑 S 밁 δ 멂 Ś 밁 S 밁 S 밁 5 멼 밁 문 밁 Matches 2594; 1874 1814 1754 1694 1634 1574 1514 1454 1394 1334 361 301 181 121 541 481 421 241 601 61 1 ATCGATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGT 60 CACCGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGT 180 GAGGAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTAT GAGGAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTAT 120 ATCGATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGGATGAAGAGGGT 1393 CAAGACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTG GTGTGGTAATTTTTTTTTTAATTTTTTAAGGTTTTGTGGTTTTAAAGAATTTTGTGTATTGTGA 300 GGCATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTG CACCGGAGGAATACGGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGT CTGAGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTG TGTCTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTC CAAGACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTG TTTTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTG TTTTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTG GTGTGGTAATTTTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGA GGCGTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGG TGTCTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTC Conservative , , Mismatches <u>.</u> Indels 0; Gaps 660 1453 1873 1693 360 1633 1573 1513 1933 600 540 1813 480 1753 420 240

2954 GGTATATGCAAAGGTGGCACTTAGGCCAGATTGCAAGATCAGCAAGATCAGCAAACTTGTAAA 3013 1681 TATCAGGAATTGTTGCTACATTTCTGGGAACGGGGCCGAGGTGGAGATAGAT	1561 CATAGAGCAGCTGACCACTTACTGGCTGCAGCCAGGGGATGATTTTTGAGGAGGCTATTAG 1620	1501 TTTTCAACAGATCAAGGATAATTGCGCTAATGAGCTTGATCTGCTGGCGCAGAAGTATTC 1560 	1441 AGAGGAGGCTAGGAATCTAGCTTTAGCTTAATGACCAGACACCGTCCTGAGTGTATTAC 1500	1381 TACAGAGGATGGGCAGGGGCTAAAGGGGGTAAAGAGGGAGCGGGGGGGCTTGTGAGGCTAC 1440				1141 TGGATTTTCTGGCCATGCATCTGTGGAGAGGCGCTTGTGAGACACAAGAATCGCCTGCTAC 1200	1081 TTTTGAGTTTTATAAAGGATAAATGGAGCGAAGAAACCCATCTGAGCGGGGGGTACCTGC 1140		961 TGAAATCCTGTGGTGAGCTGTTTGAATCTTTGAATCTGGGTCACCAGGCGCTTTTCCAAG 1020	TACAAGTGGGAATTTGAAGAGCTTT               TACAAGTGGGAATTTGAAGAGCTTT	841 ACTTGCTGGAACAGAGCTCTAACAGTACCTCTTGGTTTTGGAGGTTTCTGTGGGGCTCAT 900	781 TGGTTACATCTGACCTCATGGAGGCTTGGGAGTGTTTTGGAAGATTTTTCTGCTGTGCGTA 840	721 TGCATGGCGTGTTAAATGGGGCGGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCT 780	661 CGCCTTTGTTTGCTGAATGAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACT 720	
XX DT 04-DEC-2003 (first entry) XX DE Chromosomal insertion pGRE5-2.E1. XX	RESULT 6 ADB75124 ID ADB75124 standard; DNA; 7607 BP. XX AC ADB75124;	Qy 2581 AGATACAGATTGAG 2594 	2521 3854	CTGCC	2401 CATGACCATGAAGATCTGGAAGGTGCTGAGGTACGATGAGACCCGCACCAGGTGCAGACC	Qy 2341 CACTAAGATATTGCTTGAGCCCGAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTTTGA 2400	Qy 2281 TTCCTTGCATTTGGGTAACAGGAGGGGGGTGTTCCTACCTA	Qy 2221 CGTAGCCAGCCACTCTCGCAAGGCCTGGCCACTGTTTTGAGCATAACATACTGACCCGCTG 2280	2161 3494	2101 CATGCTAGTGAAAAGCGTGGCTGTGATTAAGCATAACATGGTATGTGGCAACTGCGAGGA 		1981 GTGTCGCCCAAAAGCAGGGCTTCAATTAAGAAATGCCTCTTTGAAAGGTGTACCTTGGG		1861 CAATACCAACCTTATCCTACACGTGTTAAGCTTCTATGGGTTTAACAATACCTGTGGA	1801 GGTGGTTATTATGGATGTAAGGTTTACTGGCCCAATTTTAGCGGTACGGTTTTCCTGGC		Db 3014 TATCAGGAATTGTTGCTACATTTCTGGGAACGGGGCCGAGGTGGAGATAGAT

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CC The invention describes an isolated nucleic acid (I) comprising consideratively linked to the sequence, and a photoreceptor-specific converter. A Recombinant adenovirus vector (II) comprising (II) is useful corrected delivery of a gene product to the eye of a mammal which convolves administering (II) that comprises heterologous DNA encoding the convolves administering (II) that comprises heterologous DNA encoding the corrected product or resulting in expression of the gene product, where the corrected product or recombinant virus comprises a fibre protein that specifically or combinant virus comprises a fibre protein that specifically or composite in the eye. The recombinant virus comprises a fibre protein containing a sufficient portion of the N-terminus of an adenovirus type 2 or type 5 fibre protein for contraction of an adenovirus type 2 or type 5 fibre protein for corrected mucleic acid comprises a photoreceptor-specific promoter coperatively linked to a nucleic acid comprises a photoreceptor-specific product which is chosen from trophic factor, anti-apoptotic factor, gene encoding a rhodopain protein, will-type Stargards give stargards disease e.g., retinal conditions a protein that regulates expression of a photoreceptor-specific gene product. The delivery is effected for treatment of an anti-collar disease such as retinal degenerative disease e.g., retinal convacuative disease, diabetic retinopathies, retinal convacuative disease, diabetic retinopathies, retinal convacuative disease, diabetic retinopathies, retinal convacuative disease, and an adenovirus packaging signal operatively linked to the sequence. The ITRs and packaging signal correcter (II) includes photoreceptor proventers providing a means not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ophthalmological; antiinflammatory; antidiabetic; gene therapy; adenovirus inverted terminal repeat sequence; adenovirus inverted terminal repeat sequence; adenovirus packaging signal; photoreceptor-specific promoter; adenovirus type 37; adenovirus type 0 serotype; adenovirus type 2; adenovirus type 5; photoreceptor; trophic factor; anti-apoptotic factor; rhodopsin; wild-type Stargardt disease gene; STDG1; anti-cancer agent; retinal degenerative disease; retinitis pigmentosa; Stargardt's disease; diabetic retinopathy; retinal vascularisation; choroideraemia; gyrate atrophy; macular dystrophy; retinoblastoma; photoreceptor-restricted transgene expression; special procession; addressions and control of the started transgene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids comprising adenovirus inverted terminal repeat sequences, adenovirus packaging signals operatively linked to the sequences and photoreceptor-specific promoters, useful for treating retinitis pigmentosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         recombinant adenovirus vector; adenovirus type 5; E1; chromosomal insertion; ds.
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promoter. (II) includes photoreceptor promoters providing a means not only for specific targeting of expression in these cells, but also for photoreceptor-restricted transgene expression. This sequence represents chromosomal insetion found in adenoviral plasmids of the A549 lung carcinoma cell line which provide a complement of adenoviral El gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 5; Page 90-93; 106pp; English.
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TGAAATCCTGT	CCCAGGCAAAG	ACTTGCTGGAI	TGGTTACATCTGACCTCATGGAGGCTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGCGTA 	TGCATGGCGTGTTAAATGGGGCGGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCT	CGCCTTTGTTTGCTGAATGAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACT	ACTTGAGCTGTAAACGCCCCAGGCCATAAGGTGTAAACCTGTGATTGCGTGTGTGGTTAA 	GGCGTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGG 	CTGAGATACAC	TGTCTAGAGAATGCAATAGTAGTACGATAGCTGTGACTCCGGTCCTTCTAACACACCCTC 	CAAGACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTG	TITITIAAAAGGICCTGIGICTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTG 	GTGTGGTAATTTTTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGA 	GGCATGTTTGT	CACCGGAGGAATACGGGGGACCCAGATATTATGTGTTTCGCTTTGCTATATGAGGACCTGT	GAGGAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTAT	ATCGATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGT 	100. imilarity 100. ; Conservative	7607 BP; 18
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The invention describes an isolated nucleic acid molecule (I) comprising CC an adenovirus tripartite leader (TPL) nucleotide, the TPL nucleotide CC sequence comprising a first and second different TPL exons or first, CC second and third same or different TPL exons, the TPL exons chosen from CC complete or partial TPL exon 1, complete TPL exon 2 and complete TPL exon 2.

CC animal, or for producing a putless adenoviral vector particle. A CC recombinant adenovirus particle (II) is useful for delivery of an CC exogenous gene to a target cell which involves contacting the cell with an amount of (II) sufficient to infect the cell. A helper-independent CC producing an adenovirus vector particle containing (III) which involves contacting the cell with involves contacting the cell with involves contacting the cell with involves contacting an adenovirus vector particle containing (III) which involves contacting and packaging cell line which is deficient in expressing containing particles and harvesting the particle produced by the cell containing particles and harvesting the particle produced by the cell involves complementing a missing fiber gene of (III) or helper-dependent fiber prosecutory gene of (III) or helper-dependent cells a fiber gene from a different adenovirus vector genome by expressing in packaging cells a fiber gene from a different adenovirus such as hereditary gene therapy. (II) is useful for treating diseases such as hereditary of diserupt HIV infection. This sequence represents construct GRE5-2.E1, a plasmid inserted into the chromosomal DNA of lung carcinoma line A59.
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The present sequence is that of a pDBX/B1 plasmid used in the method of CC the invention. The plasmid contains an adenovirus type 5 (AD5) E1 CC regulatory gene controlled by a mouse mammary tumour virus (MMTV) CC promoter. The invention provides adenoviral vectors having deletions of CC all or part of various gene sequences encoding adenoviral structural CC proteins and/or early region proteins. Deletions in these proteins would CC allow a reduced risk of wild-type virus contamination and would also CC diagnostic and therapeutic applications. The adenoviral vectors having CC deletions in the structural and/or early gene regions are produced by CC cellular complementation of these adenoviral genes. Therefore, the CC pDEX/B1 plasmid was used as a complementation plasmid which was CC introduced into a host cell line where parts of the B1 gene region would CC be stably inserted into the host cell chromosomes. The resulting E1 gene CC discasses (e.g. Huntington's disease, Tay-Sachs (e.g. tumours), genetic CC diseases (e.g. Huntington's disease, They can also be used for disease), or infections (e.g. HIV infection). They can also be used for CC controduction of biologically active proteins. (Updated on 25-MAR-CC 2003 to correct PI field.)
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New nucleic acid comprising an adenovirus tripartite leader nucleotide for producing high-capacity and targeted vectors for adenovirus-based
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The specification describes a nucleic acid molecule comprising an adenovirus (AV) tripartite leader (TPL) nucleotide with a sequence comprising two different TPL exons or three same or different TPL exons. The nucleic acid is used to produce an adenovirus vector particle, deliver an exogenous gene to a target cell, pseudotype recombinant viral vectors, target an adenovirus vector to a cell, produce a modified adenovirus, deliver a heterologous gene to an animal and produce a gutless adenoviral vector particle. The present sequence represents an El expressing plasmid, which is used for complementation of El-gene deleted
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Length

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61 GAGGAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTAT 1 ATCGATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGACGAGGATGAAGAGGGT TGCATGGCGTGTTAAATGGGGCGGGGCTTAAAGGGTATATAATGCGCCCGTGGGCTAATCT GGCGTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGG CTGAGATACACCCGGTGGTCCCCCCTGTGCCCCCATTAAACCAGTTGCCGTGAGAGTTTGGTG GTGTGGTAATTTTTTTTTTAATTTTTTACAGTTTTGTGGTTTTAAAGAATTTTGTATTGTGA CGCCTTTGTTTGCTGAATGAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACT TGTCTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTC CAAGACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTG CAAGACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTG TTTTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTG GTGTGGTAATTTTTTTTAATTTTTTACAGTTTTGTGGTTTTAAAGAATTTTTGTATTGTGA 300 GCATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTG GGCATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGGTGTTG CACCGGAGGAATACGGGGGACCCAGATATTATGTGTTTCGCTTTTGCTATATGAGGACCTGT ATCGATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGT 1884 GGCGTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGG CTGAGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTG TGTCTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCCTC TTTTTTAAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTG CACCGGAGGAATACGGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGT GAGGAGTTTGTGTTAGATTATGTGGAGCACCCCCGGGCACGGTTGCAGGTCTTGTCATTAT Mismatches 0, Indels 0, Gaps 2544 2484 180 2604 720 660 2424 600 2364 540 2304 480 2244 420 2184 360 2124 2064 240 2004 1944 120 60 0

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                                                                                               CATGACCATGAAGATCTGGAAGGTGCTGAGGTACGATGAGACCCGCACCAGGTGCAGACCCGTGACCATGAAGATCTGGAAGGTGCTGAGGTGCTGAGGTACGATGAGCCCGCACCAGGTGCAGACCCATGAAGATCTGGAAGGTGCTGAGGTACGATGAGACCCGCACCAGGTGCAGACC
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                                                                                                             Adenovirus; inverter terminal repeat sequence; ITRS; ocular disease; fiber protein; photoreceptor; rhodopsin; stargardt disease gene; STD opthalmological; antiinflammatory; antidiabetic; cytostatic;
                                                                                                                                                                                                                                                            ABA94256 standard;
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                                                                      Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC (AV) invertien provides an isolated polynucleotide comprising adenovirus CC (AV) inverter terminal repeat sequences (ITRS), AV packaging signal CC operatively linked to ITRS and a photoreceptor-specific promoter. A CC recombinant AV vector (AVV) comprising the polynucleotide is useful for CC vitreous cavity), for treating an ocular disease, e.g., rethnal CC degenerative disease, retinitis pigmentosa, Stargardt's disease, diabetic critinopathies, retinal vascularizations, and retinoblastoma, of a mammal CC preferably human. The AAV comprises a fiber protein that specifically or CC selectively binds to receptors that are expressed on cells (preferably CC photoreceptors in the eye). Preferably, the recombinant virus comprise a CC fiber protein from an adenovirus type D subgroup or is a chimeric protein CC containing a portion of the N-terminus of an adenovirus type 2 or type 5 cc penton, and the therapeutic product is a trophic factor, an anti-CC apoptotic factor, gene encoding a rhodopsin protein, a wild-type CC stargardt disease gene (STDGI), an anti-cancer agent and a protein that cregulates expression of a photoreceptor specific gene product. The viral cucleic acid of AAV comprises ITRS and packaging signal derived from AAV subgroup B or C, especially an AV type 2 or type 5. AAV is also useful CC protein or its portion, and selectively transduces photoreceptors and CC delivers a gene product encoded by AAV. The present sequence represents CC an expression plasmid pdEX/El containing the adenovirus El gene
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Matches 2594
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(NEME/)
(VSEG/)
(FRIE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotide for making vectors, useful for treating ocular diseases, e.g., retinitis pigmentosa, comprises adenovirus inverter terminal repeat sequences, packaging signal and photoreceptor-specific promoter.
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The invention describes an isolated nucleic acid (I) comprising CC adenovirus inverted terminal repeat sequence, an adenovirus packaging CC signal operatively linked to the sequence, and a photoreceptor-specific CC promoter. A Recombinant adenovirus vector (II) comprising (I) is useful CC involves administering (II) that comprises heterologous DNA encoding the CC involves administering (II) that comprises betterologous DNA encoding the CC gene product or resulting in expression of the gene product, where the recombinant virus comprises a fibre protein that specifically or CC gelectively binds to receptors that are expressed on cells which are CC photoreceptors, in the eye. The recombinant virus comprises a fibre protein which is an adenovirus type 37, from an adenovirus type D grotein which is an adenovirus type 37 from an adenovirus type D containing a sufficient portion CC of the N-terminus of an adenovirus type 2 or type 5 fibre protein for interaction with an adenovirus type 2 or type 5 penton, and a sufficient portion of an adenovirus serotype D knob portion of the fiber for call comprises a photoreceptor-specific promoter encapsulated nucleic acid comprises a photoreceptor-specific promoter operatively linked to a nucleic acid comprising the therapeutic product

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids comprising adenovirus inverted terminal repeat sequences, adenovirus packaging signals operatively linked to the sequences and photoreceptor-specific promoters, useful for treating retinitis pigmentosa.
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CC which is chosen from trophic factor, anti-apoptotic factor, gene encoding CC a rhodopsin protein, wild-type Stargardt disease gene (STDG1), an anti-cancer agent and a protein that regulates expression of a photoreceptor-specific gene product. The delivery is effected for treatment of an CC ocular disease such as retinal degenerative disease e.g., retinitis CC pigmentosa, Stargardt's disease, diabetic retinopathies, retinal CC vascularisation, choroideraemia, gyrate atrophy or macular dystrophy or retinoblastoma inherited and acquired retinal and neovascular degenerative diseases. The viral nucleic acid comprises an adenovirus converted terminal repeat (ITR) sequence, and an adenovirus packaging CC inverted terminal repeat (ITR) sequence, and an adenovirus type 2 or converted from an adenovirus sequence. The ITRs and packaging signal CC are derived from an adenovirus sequence aphotoreceptor-specific promoter. (II) includes photoreceptor promoters providing a means not CC only for specific targeting of expression in these cells, but also for photoreceptor-restricted transgene expression. This sequence represents CC an adenovirus 11-expressing plasmid for complementation of an E1-gene-
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cytostatic; anti-HIV; gene therapy; HIV gene expression inhibitor; HIV gene expression activation; adenovirus tripartite leader; TPL; gutless adenoviral vector particle; helper-independent fiberless recombinant adenovirus vector; packaging cell line; pseudotyping; adenovirus vector; gene therapy hereditary disorder; tumour; HIV infection; El transcription unit; El-gene-deleted adenoviruses; hygromycin resistance; ds; circular;
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The invention describes an isolated nucleic acid molecule (I) comprising comparising a first and second different TPL exons or first, sequence comprising a first and second different TPL exons or first, complete or partial TPL exon 1, complete TPL exon 2 and complete TPL exon 2.

(C) animal, or for producing a putless adenoviral vector particle. A complete TPL exon 2 and complete TPL exon 2.

(C) animal, or for producing a putless adenoviral vector particle. A complete TPL exon 2 and complete TPL exon 2 a
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Best Local
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Skripchenko Y;
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(HALL/)
(STEV/)
(SKRI/)
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26-JUN-2000; 2000US-00423783
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SKRIPCHENKO Y.
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                                             GAGGAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTAT 120
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Pred. No. 0;
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ng gutless adenoviral vector
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GAGGAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTAT

1884 60

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2281 TTCCTTGCGTTACAGGAGGGGGTGTTCCTACCAATGCAATTTGAGTCA 2340	1201 TGTTGTCTTCCGTCCGCCGGGGATAATACCGACGGAGGAGCAGCAGCAGCAGCAGGAGG 1260	Ś
2221 CGTAGCCAGCCACTCTCGCAAGGCCTGGCCAGTGTTTGAGCATAACATACTGACCCGCTG 2280	1141 TGGATTTTCTGGCCATGCATCTGTGGAGAGGGGTTGTGAGACACAAGAATCGCCTGCTAC	B 8
3985 CAGGGCCTCTCAGATGCTGACCTGCTCGGACGGCAACTGTCACCTGCTGAAGACCATTCA 4044	1081 TTTTGAGTTTTATAAAGGATAAATGGAGCGAAGAAACCCATCTGAGCGGGGGTACCTGC 1140	B 성
CATGGGGGGGGGGGGGGGGGGGGGGGGGAAGGGGGAACGGGGAACGGGGGG	1021 AGAAGGTCATCAAGACTTTGGATTTTTCCACACCGGGGCGCGCTGCGGGTGCTGTTGCTT 1080	B 8
301 CATGCTBAGGTAACTCCAGGGTGGGCCACAATGGGCTATGCTGGCACTGTGGTTGCTT 3924	961 TGAAATCCTGTGGTGAGCTGTTTGATTCTTTGAATCTGGGTCACCAGGGGCTTTTCCÀAG 1020 	8 <b>8</b>
GTGTCGCCCCAAAAGCAGGCTTCAATTAAGAAATGCCTCTTTGAAAGGTGTACCTTGGG 	901 CCCAGGCAAAGTTAGTCTGCAGAATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTT 960 	g Q
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CARIACCARCCITATECTACACGGTGTANGCTTCTATGGGTTAACARTACCTGTGGTGGA	781 TGGTTACATCTGACCTCATGGAGGCTTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGCGTA 840	용 <b>성</b>
	721 TGCATGGCGTGTTAAATGGGGCGGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCT 780	β & δ
	661 CGCCTTTGTTTGCTGAATGAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACT 720	B 성
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TATES A CONTRACTOR AND A CONTRACT A CONTRACT A CANTAL AND A CONTRACT AND A CON	541 GGCGTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGG 600	<u> </u>
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THE CANCAGAT CAAGGAT AA I TO COC I PAI TO AGO I TOAL CHO COCCAGAAGIA I IC	421 TGŤCTAGAGAATGCAATAGTAGGATAGGGATAGCTGTGACTCCGGTCCTTCTAACACACCTC 480	B 8
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ACAGANGA   GOCCAGOGO   ACAGANGAGAN COGGGGG   1 GAGGC	301 TITTITAAAAGGTCCTGTGTGTGAAACCTGAGCCTGAGCCAGAACCCGGAGCCTG 360 	<u> </u>
	241 GTGTGGTAATTTTTTTTTTAATTTTTACAGTTTTGTGGTTTTAAAGAATTTTGTATTGTGA 300 	<u> </u>
AGECANDE GOUGE OF CONTROL OF CONT	181 GGCATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTG	B 8
	121 CACCGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTTGCTATATGAGGACCTGT 180	9d 6

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RESULT 13
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 The present sequence is that of a pE1/Fiber plasmid used in the method of the invention. The plasmid contains an adenovirus type 5 (AD5) fiber gene controlled by a CMV promoter, an AD5 El gene and a pMAM backbone. The
                                                                                                                                                                                                                                                                                                                                                                                              Circular; adenovirus type 5; pE1/Fiber plasmid; structural protein; complementation; fiber protein; gene therapy; HIV; tumour; AD5; early gene; Huntington's disease; Tay-Sachs disease; sickle cell di E1 regulatory protein; ds.
                                                                                                    WPI; 1998-230709/20
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                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                  Adenoviral vectors - which lack DNA encoding for structural fibre protein used particularly for gene therapy.
                                                                                                                          Nemerow
                                                                                                                                                                                 25-SEP-1996;
                                                                                                                                                                                                     24-SEP-1997;
                                                                                                                                                                                                                                                  WO9813499-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete sequence
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29-SEP-1998
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SCRIPPS RES INST
                                            1; Page 112-131; 170pp; English.
                                                                                                                        GR, Von Seggern DJ;
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                                                                                                                                                                                                                                                                 /*tag= a
/note= "AD5 El regulatory gene"
complement (10922. .14223)
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/note= "AD5 fiber gene consisting of a CMV promoter;
end of this gene"
                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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Best Local Similarity 100.
Matches 2594; Conservative
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CC invention provides adenoviral vectors having deletions of all or part of C various gene sequences encoding adenoviral structural proteins and/or CC early region proteins. Deletions in these proteins would allow a reduced CC risk of wild-type virus contamination and would also allow packaging of C foreign DNA in such vectors for a variety of distinct and therapeutic CC applications. The adenoviral vectors having deletions in the structural CC and/or early gene regions are produced by cellular complementation of C these adenoviral genes. Therefore, the pgl/Fiber plasmid was used as a CC complementation plasmid which was introduced into a host cell line where CC parts of the fiber and El gene region would be stably inserted into the host cell chromosomes. The resulting El/fiber gene deficient plasmid can be used as a gene delivery vector. The vectors can be used for diagnosis C or gene therapy, e.g. for treating conditions characterised by hyper-CC disease, Tay-Sachs disease, or sickle cell diseases (e.g. Huntington's Cd disease, Tay-Sachs disease, or sickle cell disease (e.g. Huntington's C disease, Tay-Sachs disease, or sickle cell disease), or infections (e.g. timours), genetic disease (e.g. Huntington's C disease, Tay-Sachs disease, or sickle cell disease), or infections (e.g. timours), genetic disease (e.g. Huntington's C disease), and the contraction of contract PI or field's cally active proteins. (Updated on 25-MAR-2003 to correct PI
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100.0%; Score 2594; 100.0%; Pred. No. 0; tive 0; Mismatches 멂 0; 2; Length Indels 0 0

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                                                                                                           CTGCGAGTGTGGCGGTAAACATATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGA 2520
                                                                                                                                                                                         CATGACCATGAAGATCTGGAAGGTGCTGAGGTACGATGAGACCCGCACCAGGTGCAGACC 2460
                                                                                                                                                                                                                                           CACTAAGATATTGCTTGAGCCCGAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTTTGA 2400
                                                                                                                                                                                                                                                                                                   TTCCTTGCATTTGGGTAACAGGAGGGGGGTGTTCCTACCTTACCAATGCAATTTGAGTCA 2340
                                                                                                                                                                                                                                                                                                                                                           CGTAGCCAGCCACTCTCGCAAGGCCTGGCCAGTGTTTTGAGCATAACATACTGACCCGCTG
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                 AGATACAGATTGAG 2594
                                                     GCTGAGGCCCGATCACTTGGTGCTGGCCTGCACCCGCGCTGAGTTTGGCTCTAGCGATGA
                                                                      GCTGAGGCCCGATCACTTGGTGCTGGCCTGCACCCCGCGCTGAGTTTGGCTCTAGCGATGA 2580
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                                                                                                                                                                                                                                                                         Synthetic
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                                                                                                                                                                              Human adenovirus type
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Query Match 100.0%; Score 2594; Best Local Similarity 100.0%; Pred. No. 0; Matches 2594; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The specification describes a nucleic acid molecule comprising an adenovirus (AV) tripartite leader (TPL) nucleotide with a sequence comprising two different TPL exons or three same or different TPL exons. The nucleic acid is used to produce an adenovirus vector particle, deliver an exogenous gene to a target cell, pseudotype recombinant viral vectors, target an adenovirus vector to a cell, produce a modified denovirus, deliver a heterologous gene to an animal and produce a gutless adenoviral vector particle. The present sequence represents a El/fiber-expressing plasmid, which was used for complementation of El/fiber-gene deleted adenoviruses
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Adenovirus; inverter terminal repeat sequence; ITRS; ocular disease; fiber protein; photoreceptor; rhodopsin; stargardt disease gene; STD opthalmological; antiinflammatory; antidiabetic; cytostatic; gene therapy; ss.
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Polynucleotide for making vectors, useful for treating ocular diseases, e.g., retinitis pigmentosa, comprises adenovirus inverter terminal repeat sequences, packaging signal and photoreceptor-specific promoter.

Example 1; Page 114-118; 149pp; English.

The invention provides an isolated polynucleotide comprising adenovirus (AV) inverter terminal repeat sequences (ITRS), AV packaging signal CC (AV) inverter terminal repeat sequences (ITRS), AV packaging signal CC operatively linked to ITRS and a photoreceptor-specific promoter. A CC recombinant AV vector (AVV) comprising the polynucleotide is useful for the cy citreous cavity), for treating an ocular disease, e.g., retinal CC vitreous cavity), for treating an ocular disease, e.g., retinal CC retinopathies, retinal vascularizations, and retinoblastoma, of a mammal CC retinopathies, retinal vascularizations, and retinoblastoma, of a mammal CC preferably human. The AAV comprises a fiber protein that specifically or CC selectively binds to receptors that are expressed on cells (preferably photoreceptors in the eye). Preferably, the recombinant virus comprise a CC fiber protein from an adenovirus type D subgroup or is a chimeric protein CC containing a portion of the N-terminus of an adenovirus type 2 or type 5 cc penton, and the therapeutic product is a trophic factor, an anti-CC apoptotic factor, gene encoding a rhodopsin protein, a wild-type CC stargard disease gene (STDG1), an anti-cancer agent and a protein that CC regulates expression of a photoreceptor specific gene product. The viral nucleic acid of AAV comprises ITRS and packaging signal derived from AAV comprises a feet therapy, where the vector comprises an AV type 37 fiber CC protein or its portion, and selectively transduces photoreceptors and CC delivers a gene product encoded by AAV. The present sequence represents comprises in protein plasmid pEI/Fiber containing the adenovirus E1 and Fiber

Sequence 14455 BP; 3698 A; 3271 C; 3565 G; 3921 T; 0 U; 0 Other;

밁 á Query Match Best Local S Matches 2594 1825 ш Similarity ATCGATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGT ATCGATCTTACCTGCCACGAGGCTGGCTTTCCCACCCAGTGACGACGACGAGGATGAAGAGGGT 100.0%; ilarity 100.0%; Conservative 0 0 Score 2594; Pred. No. 0; 0; Mismatches В 0 6 Length Indels 14455; 0 Gaps 1884 60 0

RESULT 15 ABA94259 ID ABA94259

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ALIGNMENTS

## TITLE JOURNAL COMMENT REFERENCE AUTHORS KEYWORDS SOURCE ORGANISM RESULT 1 BM655780 LOCUS ORIGIN FEATURES VERSION ACCESSION DEFINITION source Seq primer: M13 Reverse. Location/Qualifiers 45 w. Gude Dr., Rockville, Tel: 2404533151 Fax: 2404534580 1 (bases 1 to 648), Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L. Celera Anopheles gambiae EST project Unpublished (2002) Anopheles gambiae (African malaria mosquito) Anopheles gambiae Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; BM655780 648 bp mRNA linear EST 26-FEB-2002 17000687386917 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone 13600449669374 5', mRNA sequence Email: HoltRA@celera.com Plate: NU01004A9S row: N Contact: Holt R.A. BM655780.1 GI:18955291 Celera Genomics /lab host="unity" /lab host="unity" /lab host="unity" /lab host="Not1; Whole /lote="Vector: pSport1; Site 1: Sal1; Site 2: Not1; Whole /lote="Vector: pSport1; Site 1: Sal1; Site 2: Not1; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Passarch and Reference Reagent Resource Center chromosome) " /organism="Anopheles gambiae" /mol\_type="mRNA" /strain="RSP-ST (Reduced susc dev\_stage="Adult" lab\_host="DH10b" /db\_xref="taxon:7165" /clone="19600449669374" . .648 row: M Score 615.8; DB 4; Pred. No. 8.7e-156; MD 20850, USA column: susc. 20 to Permethrin std.

Query Match Best Local Similarity

23.7%; 97.7%;

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Email: graeme@helix.nih.gov
Plate: 18 row: c column:
Seq primer: M13RP1 reverse;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mu
1 (Dases 1 to 625)
Ida, H., Boylan, S., Weigel, A., Smit-McBride, Z., Chao, A.,
Buchoff, P., Wistow, G. and Hjolmeland, L.
Expressed sequence tag analysis of mouse RPE/choroid
Unpublished (2004)
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 CGGCGGCGGCAGGAGCCCATGGA 1296
                                                                            TCCGTCCGCCCGGCGATAATACCGACGAGGAGGAGCAGCAGCAGCAGGAGGAGGAAGCCAGG 1268
                                                                                                                                              CTGGCCATGCATCTGTGGAGAGCGGTTGTGAGACACAAGAATCGCCTGCTACTGTTGTCT 1208
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/lab host="EMDH10B"
/lab host="EMDH10B"
/clone_lib="Mouse RPE/choroid, unamplified: mi/mj"
/clone_lib="Mouse RPE/choroid, the foliation of the superScript plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adapter [5'-pGACTAGTTCTAGATCGCGAGGGGCGCCC(T)15-3']. cDNA was cloned in Not I/Sal I sites. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57B16J"
/db_xref="taxon:10090"
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Pred. No. 1.6e-149;
0; Mismatches 12;
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Ilsaue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-goares@wiiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-21, >AT_rich#Low_complexity (matched compliment)
Seq primer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CA307899 726 bp mRNA linear UI-H-FT1-bib-a-23-0-UI.sl NCI_CGAP_FT1 Homo sapiens UI-H-FT1-bib-a-23-0-UI 3', mRNA sequence.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; Staph aureus moi 10, 24 hours; Klebsiella moi 10, 3 hours; Staph aureus moi 10, 24 hours; Klebsiella vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; Wt adenovirus moi 500, 3 hours; Wt adenovirus wt adenovirus + LPS 24 hours; Wt adenovirus + LPS 3 hours; Wt adenovirus + LPS 24 hours; Wt adenovirus + LPS 3 hours; Wt adenovirus + LPS 3 hours; Wt adenovirus + LPS 3 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; Wt adenovirus + LPS 3 hours; Ht adenovirus + LPS 24 hours; Wt adenovirus hours; Nours; Nours; Adenovirus + LPS 3 hours; Ht adenovirus + L
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/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages
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/db_xref="taxon:9606"
/clone="UI-H-FT1-bib-a-23-0-UI"
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/lab_host="DH10B (Life Technologies)"
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                                                                                                                              Homo sapiens (human)
Homo sapiens
                                                                                Eukaryota, Metazoa, Chordata, Mammalia, Eutheria, Primates,
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TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"
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61 GAGGAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTAT 120 CD370352 750 bp mRNA linear UI-H-FT1-bkb-j-17-0-UI.s1 NCI CGAP FT1 Homo sapiens UI-H-FT1-bkb-j-17-0-UI 3', mRNA sequence. CD370352 CD370352.1 GI:31154442 EST. 1 (bases 1 to 750) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anat CGCCTTTGTTTGCTGAATGAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAA 718 GGCGTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGG CTGAGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTG CACCGGAGGAATACGGGGGACCCAGATATTATGTGTTTCGCTTTTGCTATATGAGGACCTGT 180 ATCGATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGACGAGGATGAAGAGGGT GGCGTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGG 135 CTGAGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTG TGTCTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTC TGTCTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTC CAAGACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTG CAAGACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTG TTTTTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTG 360 GTGTGGTAATTTTTTTTTAATTTTTACAGTTTTGTGGTTTTAAAGAATTTTTGTATTGTGA 300 GGCATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTG 240 CACCGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGT GAGGAGTTTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTAT ATCGATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGT CGCCTTTGTTTGCTGAATGAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAA 17 -----GTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTG Score 476; DB 6; Pred. No. 9.7e-118; 0; Mismatches 0; Craniata; Vertebrata; Catarrhini; Hominidae Length Anatomy Project (CGAP) Indels 116; cDNA clone Euteleostomi;
; Homo. Gaps 600 195 540 255 480 315 420 375 439 499 559 423

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Tissue Procurement: Dr. Gary M. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soaree, University of CDNA Library Arrayed by: Dr. M. Bento Soaree, University of I
DNA Sequencing by: Dr. M. Bento Soaree, University of Iowa
Clone Diatribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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                                            CACCGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGT 180
                                                                                                                                                          GAGGAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTAT 499
                                                                                                                                                                                                           GAGGAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTAT 120
CACCGGAGGAATACGGGGGACCCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGT
                                                                                                                                                                                                                                                                                                                     ATCGATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGT
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/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples challenged with different conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions of the conditi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
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/clone="UI-H-FT1-bkb-j-17-0-UI"
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mol_type="mRNA"
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Pred. No. 9.8e-118;
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                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
Tissue Procurement: Dr. Gary W. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
Clone Distribution: Distribution/cgap.html
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Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
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CD742927.1 GI:32293777
EST.
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OUI-H-FT1-bka-m-09-0-UI.sl NCI CGAP FT1 Homo sapiens cDNA clone
UI-H-FT1-bka-m-09-0-UI 3', mRNA sequence.
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Bldg. 31 Rm10A07 Bethesda, MD 20892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 766)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGCCTTTGTTTGCTGAATGAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAA 718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTCTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACCTC
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                                                                                                                                                                                                                                    primer: M13 FORWARD
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                       University of Iowa
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195

255 480 315 375

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Query Match 18.4%; Score 476; DB 6; Length 766; Best Local Similarity 83.8%; Pred. No. 9.9e-118; Gaps
                                              361 CAAGACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTG 420
                                                                                                                                                                                                     301 TTTTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAAACCGGAGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              498 CACCGGAGGAATACGGGGGACCCAGATATTATGTGTTTCGCTTTTGCTATATGAGGACCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 CACCGGAGGAATACGGGGGACCCCAGATATTATGTGTTCGCTTTTGCTATATGAGGACCTGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         558 GAGGAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         618 ATCGATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGT 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GAGGAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATCGATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGAGGAGGAGGAGGGT 60
                                                                                                                                                                                                                                                                                                                                                                                                       GTGTGGTAATTTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTG 240
CAAGACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="MCI CGAP FT1"

/clone lib="MCI CGAP FT1"

/note="Organ: Lung; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site]: Econ I; Site_2: Not I; NCI CGAP FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 24 hours; control 24 hours; LPS 100 ng/ml, 24 hours; Staph aureus moi 10, 3 hours; Klebsiella moi 10, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Klebsiella vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenovirus moi 500, 3 hours; Adenovirus moi 500, 3 hours; Adenovirus + LPS 3 hours; Ad adenovirus moi 500, 24 hours; Adenovirus + LPS 3 hours; Ad according to Bonaldo, Lennon and Sorres, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Duable stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GCCCANGCGG. The tissue was provided by Dr. Gary W.

Than Tight-Human Lung Alvolated by Dr. Gary W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAG_SEQ=GCCATGCCG"
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/tisuse="Pe="Alveolar Macrophage"
/dev stage="Adult"
/lab_host="DH10B (Life_Technologies)"
                                                                                                                                                               -GTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTG
315
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ORIGIN

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	FEATURES source	JOURNAL COMMENT	REFERENCE AUTHORS TITLE	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 6 CA306892/c LOCUS DEFINITION	<i>Qy</i> 6	Оу 6 рь 1	Qу 5 рь 1	Оу . 4	Qy 4
/organism="nomo sepiens" /mol type="manNa" /mol type="manNa" /mol type="manNa" /clome="UI"+-FT1-bht-p-24-0-UI" /clsue type="hlveolar Macrophage" /clsue type="hlveolar Macrophage" /lab host="DH10B (Life Technologies)" /lab host="DH10B (Life Technologies)" /clome lb="NCI CGAP FT1" /clome lb="NCI CGAP FT1" /clome lb="NCI CGAP FT1" /clome lb="nci CGAP FT1" /note="Organ: Lung; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site 1: ECOR 1; Site 2: Not 1; NCI CGAP FT1 is a normalized CDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were amixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages were booled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; PMA 10 ng/ml, 3 hours; Rlebsiella moi 10, 3 hours; Klebsiella moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral		Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs -r@mail.nih.gov Tissue Procurement: Dr. Gary W. Hunninghake, U of I CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu Seq primer: M13 FORWARD POLYA-yes.	Mammalia, Butherla; Primates, Catarrhini; Hominidae; Homo.  1 (bases 1 to 743)  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	UI-H-FT1-bht-p-24-0-UI 3', mRNA sequence. CA306892 CA306892.1 GI:24469946 EST. Homo sapiens (human) Homo sapiens (human) Homo sapiens Merazoa. Chordata. Craniata. Vartebrata. Esteleogrami.	CA306892 743 bp. mRNA linear EST 05-AUG-2004 UI-H-FT1-bht-p-24-0-UI.s1 NCI CCAP FT1 Homo sapiens cDNA clone	661 CGCCTTTGTTTGCTGAATGAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAA 718 	501 ACTTGAGCTGTAAACGCCCCAGGCCATAAGGTGTAAACCTGTGATTGCGTGTGTGT	41 GGCGTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGG 600 	481 CTGAGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTG 540	421 TGTCTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTC 480

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Query Match
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CGCCTTTGTTTGCTGAATGAGTTGATGTAAGTTTAATAAA-GGGTGAGATAATGTTTTAAC 719
                                                                                                                                                                                                                                                                                                                                                                               CTGAGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTG 540
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                                                                                                                                               ACTTGAGCTGTAAACGCCCCAGGCCATAAGGTGTAAACCTGTGATTGCGTGTGTTGAA
                                                                                                                                                                                                                                                                           GGCGTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGG 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTCTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCCTC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAAGACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTG
                                                                                                                                                                                                               GGCGTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGG
                                                                                                                                                                                                                                                                                                                                          CTGAGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTCTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTC 262
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TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_EGGCATGCCG"
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Pred. No. 6.1e-116;
0; Mismatches 1;
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
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UI-H-FT1-bjz-n-11-0-UI.s1 NCI CGAP FT1 Homo sapiens cDNA clone
UI-H-FT1-bjz-n-11-0-UI 3', mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 602)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP);
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            /(alone lib="While (Life Technologies)"
/(clone lib="Worl (CAPA FTI"
//clone lib="Worl (CAPA FTI"
//clo
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/db xref="taxon:9606"
/clone="UI-+FT1-bjz-n-11-0-UI"
/clone="UJ-+FT1-bjz-n-11-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B_(Life_Technologies)"
Hunninghake of the University of Iowa
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RESULT 8
BM591710
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                                                                                                                                  17000687388831 /
19600449695952 !
BM591710
Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
Eukaryota, Metazoa, Arthropoda; Hexapoda, Inse
Neoptera, Endopterygota, Diptera, Nematocera,
Anopheles.
1 (bases 1 to 337)
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A.,
                                                                                                                    BM591710.1 GI:18887571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAGTAGTACGGATAGCTGTGACTCCCGGTCCTTCTAACACCCTCCTGAGATACACCCCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGTCTAGAGAATGCAA
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83.5%;
                                                                                                                                           337 bp mRNA linear EST 25-FEB-2002
A.Gam.ad.cDNA.bloodl Anopheles gambiae cDNA clone
5', mRNA sequence.
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   Evans, C.A.,
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TITLE
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BF915148
BF915148.1
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Contact: Holt R.A.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 347)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.
                                                                                                               EST
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IL3-UT0114-041200-328-H03_1 UT0114
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                                                                         Homo sapiens
                                                                                            Homo sapiens (human)
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                                                                                                                                                                                                                                                                                             CIGIGGIGAGCIGITIGATICTITIGAATCIGGGICAC 337
                                                                                                                                                                                                                                                                                                                CTGTGGTGAGCTGTTTGATTCTTTGAATCTGGGTCAC 1004
                                                                                                                                                                                                                                                                                                                                                                                                     AAAGTTAGTCTGCAGAATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTTTGAAATC 967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clome lib="A.Gam.ad.cDNA.blood1"
/note="Vector: pSport1; Site 1: Sal1; Site 2: Not1; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen 24 hours after human blood feeding. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3. Clones available through the Malaria Research and Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="19600449695952"
/dev_stage="Adult"
/lab_host="DH10b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/strain="RSP-ST (Reduced susc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Anopheles gambiae"
/mol_type="mRNA"
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RESULT 10
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                   BF914577

IL3-UT0114-011200-362-G09_1 UT0114

sequence.

BF914577

BF914577.1 GI:12306035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-UT0114-
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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Seq primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                                             GGGCAACCTTTGGACTTGAGCTGTAAACGCCCCAGGCCATAAGGTGTAAACCTGTGATTG
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                                                                                                                                                                                                                                                                                                                                   GGGCAACCTTTGGACTTGAGCTGTAAACGCCCCAGGCCATAAGGTGTAAACCTGTGATTG
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: uterus tumor, Vector: puc18, Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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/dev_stage="Adult"
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|mol_type="mRNA"
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Pred. No. 2.8e-56;
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-UT0114-
011200-362-G99_1&t3=2000-12-01&t4=1)
Seq primer: puc ls forward
High quality sequence stop: 322.
Location/Qualifiers
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1 (bases 1 to 323)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                                                                                                                                                                                                                                                                                                               GCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACTTGAGCTGT 611
GCTTA 79
                                                                              GCTGA 676
                                                                                                                                                            AAACGCCCCAGGCCATAAGGTGTAAACCTGTGATTGCGTGTGTGGTTCTTGTTTATTGCA
                                                                                                                                                                                                                                  GCTGTGGAATGTATCGAGGACTTGCTTAACGAGTCTGGGCAACCTTTGGACTTGAGCTGT 144
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/dev_stage="Adult"
/clone lib="UT0114"
/clone lib="UT0114"
/note="Organ: uterus_tumor; Vector: pucl8; Site_1: SmaI;
/note="Corgan: uterus_tumor; Vector: pucl8; Site_1: SmaI;
/note="Corgan: uterus_tumor; Vector: pucl8; Site_1: SmaI;
/note="Organ: uterus_tumor; Vector: pucl8; Site_1: SmaI;
/note="Torgan: uterus_tumor; Vector: uterus_tumor; 
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Pred. No. 2.5e-49;
0; Mismatches 13;
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                            231; Conservative
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Seq primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Negai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.
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TGA
                                                                                                                                                                                                                                       GGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGCGTCGCCAGGC 553
                                       ACGCCCCAGGCCATAAGGTGTAAAACCTGTGATTGCGTGTGTGGTTCTTGTTTATTGCAGC
                                                                                                                                                                                                                                                                                 CAATAGTAGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTGAGATACACCC
                                                                     TGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACTTGAGCTGTAA 613
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Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: uterus tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence stop: 159.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                             8.6%; Score 223.8; DB 2; 95.1%; Pred. No. 3.3e-49;
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AUTHORS
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CD366021/c
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CD366021.1 GI:31150111
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Unpublished (1997)
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112
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2016021
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2017
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2018
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TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"
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JOURNAL COMMENT REFERENCE AUTHORS TITLE VERSION KEYWORDS SOURCE RESULT 13 CD742922/c ঠ 밁 S 밁 S 밁 S FEATURES DEFINITION ACCESSION Query Match Best Local Matches 234; ORGANISM source 2358 AGCCCGAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTTTGACATGACCATGAAGATCT 2417 671 Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
Clone Distribution: Distribution information can be found at
http://genome.ulowa.edu/distribution/cgap.html
The following repetitive elements were found in this cDNA
sequence: 546-595, > (CAG)n#Simple\_repeat (matched compliment) Tumor Gene Index
Unpublished (1997)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892 CD742922
UI-H-FT1-bka-k-23-0-UI.81 NCI\_CGAP\_FT1 Homo sapiens cDNA clone
UI-H-FT1-bka-k-23-0-UI 3', mRNA sequence. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anat Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo CD742922 Seq primer: M13 FORWARD POLYA=Yes. Similarity ACATATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGAGCTGAGGCCCGATCACT 552 TGGTGCTGGCCTGCACCCGCGCTGAGTTTGGCCTCTAGCGATGAAGATACAGATTGAG 2594 AACATATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGAGCTGAGGCCCGATCACT 2537 GGAAGGTGCTGAGGTACGATGAGACCCGCACCAGGTGCAGACCCTGCGAGTGTGGCGGTA 2477 GGAAGGTGCTGAGTNACGATGAGACCCGCACCAGGTGCAGACCCTGCGAGTGTGGCGGTA 612 AGCCCGAGAGCATGTCCAAGGT-AACCTGAACGGGGTGTTTGACATGACCATGAAGATCT (bases 1 to 667) TGGTGCTGGCCTGCACCCGCGCTGAGTTTGGCTCTAGCGATGAAGATACAGATTGAG 495 sapiens sapiens (human) Conservative /clone lib="NCI\_CGAP\_FT1"
/note="Organ: Lung; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI\_CGAP\_FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to /clone="UI-H-FT1-bka-k-23-0-UI" /tissus\_type="Alveolar Macrophage" /dev\_stage="Adult" /lab\_host="DH10B (Life\_Technologies)" /organism="Homo sapiens" /mol\_type="mRNA" /db\_xref="taxon:9606" Location/Qualifiers 8.6%; 98.7%; 0; Mismatches Score 222.4; DB 6 Pred. No. 9.8e-49; DB 6; 2 Anatomy Project (CGAP), Indels Length 741; 1, 672

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SOURCE
ORGANISM
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CD365243
CD365243 CD365243 GI:31149333
                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary M. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
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1 (bases 1 to 661)

NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP);
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Unpublished (1997)
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                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAG TISSUE=Human Lung Alveolar Macrophage TAG_LIB=UI-H-FT1
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M13 FORWARD
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97.8%;
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Pred. No. 1.8e-35;
0; Mismatches 4
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Matches

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VERSION KEYWORDS

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JOURNAL

REFERENCE

AUTHORS TITLE

DEFINITION CD365243/c

Locus RESULT 14

POLYA-Yes.

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REFERENCE
AUTHORS
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LOCUS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                 173 bp mRNA linear EST 25-FEB-2002
17000687054399 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA clone
19600449720751 5', mRNA sequence.
                                                                                                                                              Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
Eukaryota, Metazoa; Arthropoda; Hexapoda, Insecta; Pterygota;
Neoptera, Endopterygota; Diptera; Nematocera; Culicoidea;
1 (bases 1 to 173)
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L.,
Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
                                                                                                                                                                                                                                                                                                                                          BM600614.1 GI:18898718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGGTACGATGAGACCCGCACCAGGTGCAGACCCTGCGAGTGTGGCGGTAAACATATTAG
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/clone="UI-H-FT2-bjj-c-23-0-UI"
/tlssue_type="Alveolar Macrophage"
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/lab_host="DH10B (Life Technologies)"
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mol_type="mRNA"
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Tel: 2404533151
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Contact: Holt R.A.
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/note="Vector: pSport1; Site 1: Sal1; Site 2: Not1; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen 24 hours after human blood feeding. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and
                                                                                                                                                                                                                                                                                                                                                                                                                  Reference Reagent Resource Center (www.malaria.mr4.org)"
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/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std.
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lab_host="DH10b"
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clone="19600449720751"
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APPLICANT: Kochanek, Stefan
APPLICANT: Kochanek, Stefan
APPLICANT: Schiedner; Gudrun
ITITLE OF INVENTION: Permanent amniocytic cel
TITLE OF INVENTION: Production and use for
TITLE OF INVENTION: Vectors
FILE REFERENCE: 50125/007002
CURRENT FAPLICATION NUMBER: US/09/714,550
CURRENT FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: US 60/167,439
PRIOR FILING DATE: 1999-11-23
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 7090
TYPE: DNA
ORGANISM: Plasmid STK146
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                                                                                                                                                                                                                                                                                                                                                                                                        ATCGATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGT
                                 TTTTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCCAGAACCGGAGCCTG
                                                                                    GTGTGGTAATTTTTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGA
                                                                                                                                                                   GGCATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTG
                                                                                                                                                                                                                                             CACCGGAGGAATACGGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGT
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US-08-473-399B-3
US-08-473-399B-3
US-08-853-831-1
US-08-853-831-1
US-08-853-831-3
US-09-510-885-3
US-09-510-885-3
PCT-US93-09774-3
PCT-US93-09774-3
US-09-713-678-39
US-08-752-760A-1
US-08-540-077-4
US-08-540-077-2
US-08-945-424-1
US-09-714-855-5
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Minimum Maximum

Sequence:

1381 TACAGAGGATGGGCAGGGGCTAAAGGGGGTAAAGAGGGAGCGGGGGCTTGTGAGGCTAC 1440 	1321 GGGAATGAATGTTGTACAGGTGGCTGAACTGTATCCAGAACTGAGACGCATTTTGACAAT 1380 	61 AAGCCAGGCGGCGGCAGGAGCAGAGCCCATGGAACCCGAGAGCCGGCCTGGACCCTC 1	01 TGTTGTCTTCCGTCCGCCGGCGATAATACCGACGGAGGAGCAGCAGCAGCAGCAGGAGGAGGAGGAG	1 TGGATTTTCTGGCCATGCATCTGTGGAGAGCGGTTGTGAGACAAGAATCGCCTGCTAC 1	TTTTGAGTTTTATAAAGGATAAATGGAGGGAAGAAACCCATCTGAGCGGGGGGGTACCTGC 1	AGAAGGTCATCAAGACITTGGATTTTTCCACACCGGGGGGGGGTGCGGGTGCTGTTGCTT 1	1 TGAAATCCTGTGGTGAGCTGTTTGATTCTTTGAATCTGGGTCACCAGGCGCTTTTCCAAG 1	CCCAGGCAAAGTTAGTCTGCAGAATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTT 9	ACTIGCTGGAACAGAGCTCTAACAGTACCTCTTGGTTTTGGAGGTTTTCTGTGGGGCTCAT 9	1 TGGTTACATCTGACCTCATGGAGGCTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGGGTA 8	TGCATGGCGTGTTAAATGGGGCGGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCT 7	1 CGCCTTTGTTTGCTGAATGAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACT 7	recerere:	541 GGCGTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGG 600 	0 	421 TGTCTAGAGAATAGCAATAGTAAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTC 480	361 CAAGACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTG 420 
QY 2401 CIGCUMATICUS CONTRACTA A LA SALAGAMA CANCINE SALAGAMA 2220 CIGCUMATICA CONTRACTA A CANCINE SALAGAMA 2220 CIGCUMATICA CONTRACTA C	2401 CATGACCATGAAGATCTGGAAGGTCCTGAGGTACGATGAGACCCGCACCAGGTGCAGACC	2341 CACTAAGATATTGCTTGAGCCCGAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTTTGA	Qy 2281 TTCCTTGCATTTGGGTAACAGGAGGGGGGTGTTCCTACCTTACCAATGCAATTTGAGTCA 2340	Qy 2221 CGTAGCCAGCCACTCTCGCAAGGCCTGGCCAGTGTTTGAGCATAACATACTGACCCGCTG 2280	OY 2161 CAGGGCCTCTCAGATGCTGACCTGCTCGGACGCAACTGTCACCTGCTGAAGACCATTCA 2220	QY 2101 CATGCTAGTGAAAAGCGTGGCTGTGATTAAGCATAACATGGTATGTGGCAACTGCGAAGA 2160	ATCCTGTCTGAGGGTAACTCCAGGTGGGCCACAATGTGGCCTCCGACTGTGGTTGCTT	GTGTCGCCCCAAAAGCAGGGCTTCAATTAAGAAATGCCTCTTTGAAAGGTGTACCTTGGG 	OY 1921 AGCCTGGACCGATGTAAGGGTTCGGGGCTGTGCCTTTTACTGCTGCTGGAAGGGGTGGT 1980	QY 1861 CAATACCAACCTTATCCTACACGGTGTAAGCTTCTATGGGTTTAACAATACCTGTGTGGA 1920	QY 1801 GGTGGTTATTATGAATGTAAGGTTTACTGGCCCCAATTTTAGCGGTACGGTTTCCTGGC 1860	QY 1741 TAGGGTGGCCTTTAGATGTAGCATGATAAATATGTGGCCGGGGGTGCTTGGCATGGACGG 1800	QY 1681 TATCAGGAATTGTTGCTACATTTCTTGGGAACGGGGCGGAGGTTGGAGATAGAT	1621 GSTATATGCAAAGGTGGCACTTAGGCCAGATTGCAAGTACAAGATCAGCAAACTTGTAAA	1561 CATAGAGCAGCTGACCACTTACTGGCTGCAGCCAGGGGATGATTTTGAGGAGGGCTATTAG	1501 TTTCAACAGATCAAGGATAATTGCGCTAATGAGCTTGATCTGCTGGCGCAGAAGTATTC	1441 AGAGGAGGCTAGGAATCTAGCTTTAGCTTAATGACCAGACACCGTCCTGAGTGTATTAC

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ρ	ממ	δ <u>B</u>	Ŋ	B 8	B 6	5 B 8	B &	Db Qy	B &	B Q	D Q	B &	B &	B 8	B &	ρ <i>δ</i> ν	B 29	B &	g Q
1321 GGGAATGAATGTTGTACAGGTGGCTGAACTGTATCCAGAACTGAGACGCATTTTGACAAT 1380		2117 TGTTGTCTTCCGTCCGCCCGGCGATAATACCGACGAGGAGCAGCAGCAGCAGCAGCAGGAGG 2176  1261 AAGCCAGGCGGCGGCAGGAGCAGAGCCCATGGAACCCGAGAGGCCGGCC	1201 TGTTGTCTTCCGTCCGGCCGGCGATAATACCGACGGAGGAGCAGCAGCAGCAGCAGGAGG 1260	1141 TGGATTTTCTGGCCATCTGTGGAGAGCGGTTGTGAGACACAAGAATCGCCTGCTAC 1200	TITIGAGITITATAAAGGATAAATGGAGGGAAGAAACCCATCTGAGCGGGGGGTACCTGC 11	AGAAGGTCATCAAGACTTTGGATTTTTCCACACCGGGCCGCCTCCTGCGGTGCTGCTTGCT	961 TGAAATCCTGTGGTGAGCTGTTTGATTCTTTGAATCTGGGTCACCAGGCGCTTTTCCAAG 1020	901 CCCAGGCAAAGTTAGTCTGCAGAATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTT 960 	841 ACTIGCTGGAACAGAGCTCTAACAGTACCTCTTGGTTTTGGAGGTTTCTGTGGGGCTCAT 900	781 TGGTTACATCTGACCTCATGGAGGCTTGGGAGGTGTTTGGAAGATTTTTCTGCTGTGCGTA 840	721 TGCATGGCGTGTTAAATGGGGCGGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCT 780	661 CGCCTTTGTTTGCTGAATGAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACT 720 	601 ACTTGAGCTGTAAACGCCCCAGGCCATAAGGTGTAAACCTGTGATTGCGTGTGTGGTTAA 660 	541 GGCGTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGG 600	481 CTGAGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTG 540	421 TGTCTAGAGAATGCAATAGTAGGAGTAGCTGTGACTCCGGTCCTTCTAACACACCCTC 480	361 CAAGACCTACCGGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTG 420	301 TTTTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTG 360 	241 GTGTGGTAATTTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGA 300 

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46	401 CATGACCATGAAGATCTGGAAGGTGCTGAGGTACGATGAGACCCGCACCAGGTGCAGAC
2400	2341 CACTAAGATATTGCTTGAGCCCGAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTTTGA
2340 3256	2281 TTCCTTGCATTTGGGTAACAGGAGGGGGGTGTTCCTTACCTTACCAATGCAATTTGAGTCA
2280 3196	2221 CGTAGCCAGCCACTCTCGCAAGGCCTGGCCAGTGTTTGAGCATAACATACTGACCCGCTG
2220 3136	2161 CAGGGCCTCTCAGATGCTGACCTGCTCGGACGGCAACTGTCACCTGCTGAAGACCATTCA
2160 3076	2101 CATGCTAGTGAAAAGCGTGGCTGTGATTAAGCATAACATGGTATGTGGCAACTGCGAGGA
2100 3016	2041 TATCCTGTCTGAGGGTAACTCCAGGGTGCGCCACAATGTGGCCTCCGACTGTGGTTGCTT
2040 2956	1981 GTGTCGCCCAAAAGCAGGGCTTCAATTAAGAAATGCCTCTTTGAAAGGTGTACCTTGGG 
1980 2896	1921 AGCCTGGACCGATGTAAGGGTTCGGGGCTGTGCCTTTTACTGCTGCTGCAAGGGGGTGGT
1920 2836	1861 CAATACCAACCTTATCCTACACGGTGTAAGCTTCTATGGGTTTAACAATACCTGTGTGGA 
1860 2776	1801 GGTGGTTATTATGAATGTAAGGTTTTACTGGCCCCAATTTTAGCGGTACGGTTTTCCTGGC
1800 2716	1741 TAGGGTGGCCTTTAGATGTAGCATGATAAATATGTGGCCGGGGGTGCTTGGCATGGACGG
1740 2656	1681 TATCAGGAATTGTTGCTACATTTCTGGGAACGGGGCCGAGGTGGAGATAGAT
1680 2596	1621 GGTATATGCAAAGGTGGCACTTAGGCCAGATTGCAAGTACAAGATCAGCAAACTTGTAAA
1620 2536	1561 CATAGAGCAGCTGACCACTTACTGGCTGCAGCCAGGGGATGATTTTGAGGAGGCTATTAG
1560 2476	1501 TTTTCAACAGATCAAGGATAATTGCGCTAATGAGCTTGATCTGCTGGCGGAGAAGTATTC
1500 2416	1441 AGAGGAGGCTAGGAATCTAGCTTTTAGCTTAATGACCAGACACCGTCCTGAGTGTATTAC
1440 2356	1381 TACAGAGGATGGCCAGGGGCTAAAGGGGGTAAAGAGGGAGCGGGGGGGG
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NAME: INGOLIA, Diane E.

REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-02484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08735609
Patent No. 5994132
GENERAL INFORMATION:
APPLICANT: Chamberlain, Jeffre
                                                                                                                                                  Query Match 100.0%; 3
Best Local Similarity 100.0%; 1
Matches 2594; Conservative 0;
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Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Flopp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3497 AGATACAGATTGAG 3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2461 CTGCGAGTGTGGCGGTAAACATATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGA 2520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3317 CATGACCATGAAGATCTGGAAGGTGCTGAGGTACGATGAGACCCGCACCAGGTGCAGACC 3376
 977
                                                                          917
                         61 GAGGAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTAT 120
                                                                         GCTGAGGCCCGATCACTTGGTGCTGGCCTGCACCCGCGCTGAGTTTGGCCTCTAGCGATGA 2580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/735,609
FILING DATE: 23-Oct-1996
CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTGAGGCCCGATCACTTGGTGCTGGCCTGCACCCGCGCTGAGTTTGGCTCTAGCGATGA 3496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGCGAGTGTGGCGGTAAACATATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGA 3436
 GAGGAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTAT 1036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: California COUNTRY: United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 220 Montgomery Street,
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hauser, Michael A.
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                                                                                                                                                  Score 2594;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Suite 2200
                                                                                                                                                                                     DB 2;
                                                                                                                                                   0,
                                                                                                                                                                                       Length 35935;
                                                                                                                                                   Indels
                                                                                                                                                   0;
                                                                                                                                                  Gaps
                                                                          976
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1141 TGGATTTTCTGGCCATGCATCTGTGGAGAGCGGTTGTGAGACACAAGAATCGCCTGCTAC 1200	TTTTGAGTTTTATAAAGGATAAATGGAGCGAAGAAACCCATCTGAGCGGGGGGTACCTGC	AGAAGGTCATCAAGACTTTGGATTTTTCCACACCGGGGCGCGCTGCGGCTGCTGTTGCTT 1	TGAAATCCTGTGGTGAGCTGTTTGATTCTTTGAATCTGGGTCACCAGGCGCTTTTCCAAG 1	CCCAGGCAAAGTTAGTCTCCAGAATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTT CCCAGGCAAAGTTAGTCTGCAGAATTAAGGAGGATTACAAGTGGGAATTTTGAAGAGCTTT CCCAGGCAAAGTTAGTCTGCAGAATTAAGGAGGATTAAAGTGGGAATTTGAAGAGCTTTT	ACTTGCTGGAACAGAGCTCTAACAGTACCTCTTGGTTTTTGGAGGTTTCTTGGGGCTCAT	TGGTTACATCTGACCTCATGGAGGCTTGGGAGGTGTTTGGAAGATTTTTCTGCTGTGGGTA	721 TGCATGGCGTGTTAAATGGGGCGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCT 780	CGCCTTTGTTTGCTGAATGAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACT	601 ACTTGAGCTGTAAACGCCCCAGGCCATAAGGTGTAAACCTGTGATTGCGTGTGTGT	GGCGTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGG	CTGAGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTG :	421 TGTCTAGAGAATAGTAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTC 480	361 CAAGACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTG 420	301 TTTTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTG 360	241 GTGTGGTAATTTTTTTTTTTTTTACAGTTTTGTGGTTTTAAGAATTTTGTATTGTGA 300	181 GGCATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTG 240	121 CACCGGAGGAATACGGGGGACCCAGATATTATGTGTTTCGCTTTTGCTATATGAGGACCTGT 180
CGTAGCCAGCCACTCTCGCAAGGCCTGGCCAGTGTTTGAGCATAACATACTGACCCGCTG TTCCTTGCATTTGGGTAACAGGAGGGGGGGTGTTCCTACCTTACCAATGCAATTTGAGTCA	2161 CAGGG       3077 CAGGG	Qy 2101 CATGCTAGTGAAAAGCGTGGCTGTGATTAAGCATAACATGGTATGTGGCAACTGCGAGGA 2160	Qy 2041 TATCCTGTCTGAGGGTAACTCCAGGGTGCGCCACAATGTGGCCTCCGACTGTGGTTGCTT 2100	Qy 1981 GTGTCGCCCAAAAGCAGGGCTTCAATTAAGAAATGCCTCTTTGAAAGGTGTACCTTGGG 2040	Qy 1921 AGCCTGGACCGATGTAAGGGTTCGGGGCTGTGCCTTTTACTGCTGCTGGAAGGGGGTGGT 1980	Qy 1861 CAATACCAACCTTATCCTACACGGTGTAAGCTTCTATGGGTTTAACAATACCTGTGTGGA 1920	Qy 1801 GGTGGTTATTATGAATGTAAGGTTTACTGGCCCCAATTTTAGCGGTACGGTTTTCCTGGC 1860	1741 TAGGGTGGCCTTTAGATGTAGCATGATAAATATGTGGCCGGGGGTGCTTGGCATGGACGG			Qy 1561 CATAGAGCAGCTGACCACTTACTGGCTGCAGCCAGGGGATGATTTTGAGGAGGCTATTAG 1620	Qy 1501 TTTTCAACAGATCAAGGATAATTGCGCTAATGAGCTTGATCTGCTGGCGCAGAAGTATTC 1560	AGAGGAGGCTAGGAATCTAGCTTTTAGCTTAATGACCAGACACCGTCCTGAGTGTATTAC	Oy 1381 TACKANGANGGGCKAGGGGTAAAGAGGGGAAGCGGGGGCTTGTGAGGCTAC 1440	1321 GGAATGATGTTGTACAGGTGGCTGAACTGTATCCAGAACTGAGACGCATTTTGACAAT	181 ANG CAGGCGGCGGCAGGAGCAGGAGCCCATGGAACCCGAGGAGCCGGCCTGGACCCTC  2177 AAGCCAGGCGGCGGCAGGAGCAGGAGCCCATGGAACCCGAGAGCCGGCCTGGACCCTC	2117 TGTTGTCTTCCGTCCGCCCGCCGATAATACCGACGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC

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1021 AGAAGGTCATCAAGACTTTGGATTTTTCCACACCGGGCGCGCTGCGGCTGCTGTTGCTT 1080	Qy Db	Query Match 100.0%; Score 2594; DB 3; Length 35935;
	Qy	STRANDE TOPOLOC MOLECULE IS-08-379-452-
901 CCCAGGCAAAGTTAGTCTGCAGAATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTT 960 	Qy do	INFORMATION FOR SEQ ID NO: 43 SEQUENCE CHARACTERISTICS: LENGTH: 35935 base pairs TYPE: nucleic acid
841 ACTTGCTGGAACAGAGCTCTAACAGTACCTCTTGGTTTTTGGAGGTTTCTGTGGGGCTCAT 900	D Qy	; ATTORNEY/AGENT INFORMATION: ; NAME: Dadio, Susan M. ; REGISTRATION NUMBER: 40,373 ; REFERENCE/DOCKET NUMBER: 029395-002
781 TGGTTACATCTGACCTCATGGAGGCTTGGGAGGTGTTTGGAAGATTTTTCTGCTGTGCGTA 840	Qy da	FILING DATE: 27-MAY-199 PRIOR APPLICATION DATA: APPLICATION NUMBER: ETAINING DATE: 28-MAY-199
721 TGCATGGCGTGTTAAATGGGGCGGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCT 780	Qy Db	; FILING DATE: 26-JAN-1995 ; CLASSIFICATION: 435 ; PRIOR APPLICATION DATA: ; ARBELICATION UMBER: WO BCT/FEB94/00624
661 CGCCTTTGTTTGCTGAATGAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACT 720 	Qy Db	OPERATING SYSTEM: PC-DOS/MS-DOS  OPERATING SYSTEM: PC-DOS/MS-DOS  SOFTWARE: PatentIn Release #1.0, Version #1.30  CURRENT APPLICATION DATA:  APPLICATION NUMBER: 18 / 108/278 / 152
601 ACTTGAGCTGTAAACGCCCCAGGCCATAAGGTGTAAACCTGTGATTGCGTGTGTGGTTAA 660 	Qy Db	ZIP: 22314-2756  COMPUTER READABLE FORM:  MEDIUM TYPE: Flopy disk  COMPUTER I FLORY DISK
541 GGCGTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGG 600	Qy Db	STREET: 1737 King Street, Suite 500 CITY: Alexandria STATE: Virginia COUNTRY. Virginia
481 CTGAGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCCGTGAGAGTTGGTG 540	Qу	VENTION: COMPLEMENTATION LINES EQUENCES: 43 NCE ADDRESS: - NIPMS NOAME GMECKER & MATHIS I.
421 TGTCTAGAGAATGCAATAGTAGTACGATAGCTGTGACTCCGGTCCTTCTAACACACCTC 480	Qy Db	APPLICANT: IMLER, Je APPLICANT: MEHTALI, APPLICANT: PAVIRANI APPLICANT: PAVIRANI
361 CAAGACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTG 420	Qy Db	KESULT 4 US-08-379-452-43 ; Sequence 43, Application US/08379452 ; Patent No. 6040174 ; CENERAL TENERAL TROPE
301 TTTTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTG 360 	Qy dy	Db 3497 AGATACAGATTGAG 3510
241 GTGTGGTAATTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGA 300	3496 Qy	Db 3437 GCTGAGGCCCGATCACTTGGTGCCTGCCCCGCGCTGAGTTTGGCTCTAGCGATGA 3-  QY 2581 AGATACAGATTGAG 2594
1097 GGCATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTG	2580 ის	CTGGCCTGCACCCGCGCTGAGTTTGGCTCTAGCGATGA
1037 CACCGGAGGAATACGGGGGGÁCCCAGATATTATGTGTTTTGCTTATGTGAGGACCTGT 1096 181 GGCATGTTTTTTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGGGTTTTG 240	2520 Db 3436 Qy	Oy 2461 CTGCGAGTGTGGCGGTAAACATATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGA 21
CACCGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGT 180		3317 CATGACCATGAAGATCTGGAAGGTGCTGAGGTACGATGAGACCCGCACCAGGTGCAGACC
61 QAGGAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTAT 120	3316 Qy 2460 Db	Db 3257 CACTAAGATATTGCTTGAGCCCGAGGAGCATGTCCAAGGTGAACCTGAACGGGGTGTTTGA 3:  Qy 2401 CATGACCATGAAGATCTGGAAGGTGCTGAGGTACGATGAGACCCGCACCAGGTGCAGACC 2:
1 ATCGATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGT 60	3256 Qy 2400 Db	

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CATGCTAGTGAAAAGCGTGGCTGTGATTAAGCATAACATGGTATGTGGCAACTGCGAGGA CAGGGCCTCTCAGATGCTGACCTGCTCGGACGGCAACTGTCACCTGCTGAAGACCATTCA	2041 TATCCTGTCTGAGGGTAACTCCAGGGTGCGCCACAATGTGGCCTCCGACTGTGGTTGCTT 2100	1981 GTGTCGCCCCAAAAGCAGGGCTTCAATTAAGAAATGCCTCTTTGAAAGGTGTACCTTGGG 2040 	1921 AGCCTGGACCGATGTAAGGGTTCGGGGCTGTGCCTTTTTACTGCTGCTGGAAGGGGGTGGT 1980	1861 CAATACCAACCTTATCCTACACGGTGTAAGCTTCTATGGGTTTAACAATACCTGTGTGGA 1920	1801 GGTGGTTATTATGAATGTAAGGTTTACTGGCCCCAATTTTAGCGGTACGGTTTTCCTGGC 1860 	1741 TAGGGTGGCCTTTAGATGTAGCATGATAAATATGTGGCCGGGGGTGCTTGGCATGGACGG 1800	1681 TATCAGGAATTGTTGCTACATTTCTGGGAACGGGGCCGAGGTGGAGATAGAT	1621 GGTATATGCAAAGGTGGCACTTAGGCCAGATTGCAAGTACAAGATCAGCAAACTTGTAAA 1680 	1561 CATAGAGCAGCTGACCACTTACTGGCTGCAGCCAGGGGATGATTTTGAGGAGGCTATTAG 1620 -	1501 TTTTCAACAGATCAAGGATAATTGCGCTAATGAGCTTGATCTGCTGGCGCAGAAGTATTC 1560	1441 AGAGGAGGCTAGGAATCTAGCTTTTAGCTTAATGACCAGACACCGTCCTGAGTGTATTAC 1500	1381 TACAGAGGATGGGCAGGGGTAAAAGGGGGTAAAGAGGGAGCGGGGGGGG	1321 GGGAATGAATGTTGTACAGGTGGCTGAACTGTATCCAGAACTGAGACGCATTTTGACAAT 1380	1261 AAGCCAGGCGGCGGCAGGAGCAGAAGCCCATGGAACCCGAGAGCCGGCCTGGACCCTC 1320	1201 TGTTGTCTTCCGTCCGCCGGCGATAATACCGACGGAGGAGCAGCAGCAGCAGCAGCAGCAGGAGG 1260	1141 TGGATTTTCTGGCCATGCATCTGTGGAGAGGGGTTGTGAGACACAAGAATCGCCTGCTAC 1200	
TELEFAX: (415) 397-8338 ; INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: ; LENGTH: 35935 base pairs ; TYPE: nucleic acid	~ H O P	CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/735,609 FILING DATE: APTORMEY AFRET INFORMATION.	CURRENT APPLICATION DATA; APPLICATION NUMBER: US/09/315,372 FILING DATE:	‡	STATE: COUNTRY ZIP: 9	CORRESPONDENCE ADDRESS ADDRESSEE: Medlen & STREET: 220 Montgor	; AFFLICANI: HOUSE!, MICHAEL A.; APPLICANI: Kumar-Singh, Rajendra ; APPLICANT: Hartigan-O'Connor, Dennis J. ; ITILE OF INVENTION: IMPROVED ADENOVIRUS VECTORS . NUMBER OF SCOTENICS. 15	Pacenc No. GENERAL J APPLICA APPLICA	2-1 , Appli	Oy 2581 AGATACAGATYGAG 2594                Db 3497 AGATACAGATYGAG 3510	2521 GCTGAGGCCCGATC	2461 CTGCGAGTGTGGCGGTAAACATATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGA	Oy 2401 CATGACCATGAAGATCTGGAAGGTGCTGAGGTACGATGAGACCCGGCACCAGGTGCAGACC 2460	2341 CACTAAGATATTGCTTGAGCCCGACAGCATGTCCAAGGTGAACCTGAACGGGGTGTTTGA	2281 TICCTTGCATTTGGGTAACAGGAGGGGGGTTCCTTACCTTA	3137 CGTAGCCACTCTCGCAAGGCCTGGCCAGTGTTTGAGCATAACATACTGACCCGCTG	CCTCTCAGATGCTGACCTGCTCGGACGGCAACTGTCACCTGCTGAAGACCATTCA

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; STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: other nucleic DESCRIPTION: /desc = "DNA" US-09-315-372-1
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Sequence 1, Application US/09244752

Pattent No. 6063622

GENERAL INFORMATION:
APPLICANT: Chamberlain, Jeffrey S.
APPLICANT: Amalfitano, Andrea
APPLICANT: Hauser, Michael A.
APPLICANT: Hauser, Michael A.
APPLICANT: Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY. California
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US-09-244-752-1
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SOPTWARE: PATENTIN Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,752
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/735,609
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pairs
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic
DESCRIPTION: /desc = "DNA"
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REFERENCE/DOCKET NUMBER: UM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
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   TGGTTACATCTGACCTCATGGAGGCTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGCGTA 840
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                                                                                                           CGCCTTTGTTTGCTGAATGAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACT
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; COMPUTER: IBM PC compatible	5 70 72 ··	38 60	- SEE	INFO	RESULT 7 US-09-245-497-1 Sequence 1, Application US/09245497	97 AGATACAGATTGAG	3437	3377	<b>-</b>	3257	3197	3137	3077	3017	2957	2897	2837	2777

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Qy 481 CTGAGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTTGGTG 540	Db 1277 CAAGACCTACCCGCCTCTAAAATGCGCCTGCTATCCTCAGACGCCCGACATCACCTG 420  Db 1277 CAAGACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTCAAGACGCCCGACATCACCTG 1336  Db 1277 CAAGACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTG 1336  Oy 421 TGTCTAGAGAATGCAATAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTC 480  Db 1337 TGTCTAGAGAATGCAATAGTACGGATAGCTGTGACTCCCGGTCCTTCTAACACACCTC 1396	241 GIGTGGTAATTITITTATATTITTACAGTTTGGTTTAAAGAATTTTGFATTGTA	181 GGCATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTG	Oy 61 GAGAGTTYGTGTTAGATTATGTGGAGGACCCCGGGCACGGTTGCAGGTCTTGTCATTAT 120	CCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGT 60	Query Match 100.0%; Score 2594; DB 3; Length 35935; Best Local Similarity 100.0%; Pred. No. 0; Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	LENGUINE CIRCLESTICATES  LENGTH: 35935 base pairs  TYPE: nucleic acid  STRANDENNESS: double  TOPOLOGY: linear  MOLECULE TYPE: other nucleic acid  DESCRIPTION: /desc = "DNA"  US-09-245-497-1		08/735,609 <b) date:<br="" filing="">TON: E. 40,027 40,027</b)>	OPERATING SYSTEM: PC-DOS/MS-DOS SOPTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/245,497 FILING DATE: CLASSIFICATION: PRIOR APPLICATION DATA: PRIOR APPLICATION DATA:
Cy 151 CATAGGCAGCTGACCACTTACTGGCTGAGGCAGGCAGGTGATTTTGAGGAGGGTATTAG 1520  2477 CATAGAGCAGCTGACCACTTACTGGCTGAGCAGGGATGATTTTGAGGAGGGCTATTAG 2536  Qy 1621 GGTATATGCAAAGGTTGCACTTACTGGCTGAGATTGCAAGTACAAGATCAGGAGGCTATTAG 2536  Qy 1621 GGTATATGCAAAGGTTGCACTTAGGCCAGATTGCAAGTACAAGATCAGCAAACTTGTAAA 1680	2357 AGAGGAGGCTAGGAATCTAGCTTTAATGACCAGCACACCGTCCTGAGTGTATTAC 1501 TTTTCAACAGATCAAGGATAATTGCGCTAATGAGCTTGATCTGCTGGCGCAGAAGTATTC 1501 TTTTCAACAGATCAAGGATAATTGCGCTAATGAGCTTGATCTGCTGGCGCAGAAGTATTC 11	2237 1381 2297 1441	Qy 1261 AAGCCAGGCGGCGGCAGGAGCCAGAGCCCATGGAACCCGAGAGCCCGGCCTGGACCCTC 1320	2057 1201 2117	Qy 1081 TTTTGAGTTTTATAAAGGATAAATGGAGCGAAGAAACCCATCTGAGCGGGGGGGTACCTGC 1140	OY 1021 AGAAGGTCATCAAGACTTTGGATTTTTCCACACCGGGGGGGCGCTGCTGCTGTTTGCTT 1080	1817 CCCAGGCAAAGTIAGICIGCAGAATIAAGAGAGAGTIACAAGTIGGGAATIICAAGAGGCTIT 1817 CCCAGGCAAAGTTAGTCTGCAGAATTAAGAGAGATTACAAGTGGGAATTTGAAGAGCTTT  961 TGAAATCCTGTGGTGAGCTGTTTGATTCTTTGAATCTGGGTCACCAGGCGCTTTTCCAAG	841 ACTTGCTGGAACAGAGCTCTAACAGTACCTCTTGGTTTTGGAGGTTTCTGTGGGGCTCAT	Db 1637 TGCATGCCGTGTTAAATGGGCCGGGCCTTAAAGGTATATAATGCGCCCGTGGCTAATCT 1696  Qy 781 TGGTTACATCTGACCTCATGGAGGCTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGCGTA 840	Qy 661 CGCCTTTGTTTGCTGAATGAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACT 720

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RESULT 8
US-09-409-670-43
; Sequence 43, Application US/09409670
; Patent No. 6133028
; Patent No. 6133028
; PAPLICANT: IMLER, Jean-Luc
APPLICANT: MEHTALI, Majid
APPLICANT: PAVIRANI, Andrea
TITLE OF INVENTION: DEFECTIVE ADENOVIRUSES ANI
TITLE OF INVENTION: COMPLEMENTATION LINES
NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
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REGISTRATION NUMBER: 40,373
REFERENCE/DOCKET NUMBER: 0293
REFERENCE/DOCKET NUMBER: 0293
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 35935 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 100.
Matches 2594; Conservative
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APPLICATION NUMBER: US/08/379,452

FILING DATE: 26-JAN-1995

APPLICATION NUMBER: WO PCT/FR94/00624

FILING DATE: 27-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 93 06482

FILING DATE: 28-MAY-1993

ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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1737 King Street, Suite 500
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9 562-919-1	2581 AGATACAGATTCAG 2594               3497 AGATACAGATTCAG 3510	2521 GCTGAGGCCCGATCACTTGGTGCTGGCCTGCACCCGCGCTGAGTTTGGCTCTAGCGATGA 2580	CTGCGAG	CATGACCATGAAGATCTGGAAGGTGCTGAGGTACGATGAGACCCGCACCAGGTGCAGACC	2341 CACTAAGATATTGCTTGAGCCCGAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTTTGA 2400	2281 TTCCTTGCATTTGGGTAACAGGAGGGGGGTGTTCCTACCTTACCAATGCAATTTGAGTCA 2340	2221 CGTAGCCACCCACTCTCGCAAGGCCTGGCCAGTGTTTGAGCATAACATACTGACCCGCTG 2280	2161 CAGGCCTCTCACATGCTGACCTGCTCGGACGCAACTGTCACCTGCTGAAGACCATTCA 2220	CATGCTACTGAAAAGCCTGGCTGTGATTAAGCATAACATGGTATGTGGCAACTGCGAGGA 	TATCCTGTCTGAGGGTAACTCCAGGGTGCGCCACAATGTGGCCTCCGACTGTTGGTTG	GTGTCGCCCAAAAGCAGGCTTCAATTAAGAAATGCCTCTTTGAAAGGTGTACCTTGGG 	1921 AGCCTGGACCGATGTAAGGGTTCGGGGCTGTGCCTTTTACTGCTGCTGGAAGGGGGGTGGT 1980	;;;ACCTTATCCTACACGGTGTAAGCTTCTATGGGTTTAACAATACCTGTGTGGA 	1801 GGTGGTTATTATGAATGTAAGGTTTACTGGCCCCAATTTTAGCGGTACGGTTTTCCTGGC 1860	TAGGGTGGCCTTTAGATGTAGCATGATAAATATGTGGCCGGGGGTGCTTGGCATGGACGG	A CARGAMA I IG I IGC I ACAI I I C I GAGAACGAGGC CARGA I GAGAACAI ACAI ACGAGGA   A CAI A		2477 CATAGAGCAGCTGACCACTTACTGGCTGCAGCCAGGGGATGATTTTGAGGAGGCTATTAG 2536

QY 301 TTTTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTG 360	OY 241 GIGIGGIAATITITITAATITITAACAGTITITGIGGITTAAAGAATITITGIGA 300	QY 181 GGCATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGTGATAGAGTGGTTGGT	QY 121 CACCGGAGGAATACGGGGGACCCAGATATTATGTGTTTCGCTTTTGCTATATGAGGACCTGT 180	QY 61 GAGGAGTTTGTGTTAGATTATGTGGAGCACCCCGGGGCACGGTTGCAGGTCTTGTCATTAT 120	ACCTGCCACGA            ACCTGCCACGA	Query Match  100.0%; Score 2594; DB 3; Length 35935;  Best Local Similarity 100.0%; Pred. No. 0;  Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	MOLECULE TYPE: other nucleic acid  DESCRIPTION: /desc = "NNA"  SEQUENCE DESCRIPTION: SEQ ID NO: 1:  US-09-562-919-1	LENGTH: 35935 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear	TELEPHONE: (415) 705-8410 TELEPAX: (415) 397-8338 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:	NAME: INGOLIA Diane E.  REGISTRATION NUMBER: 40,027  REFERENCE/DOCKET NUMBER: UM-02484  TELECOMMINICATION INFORMATION.	PRIOR APPLICATION DATA:  APPLICATION NUMBER: US/08/735,609  FILING DATE: 23-OCC-1996  ATTORNEY JAGENT INFORMATION:	; CURRENT APPLICATION DATA: ; RAPLICATION NUMBER: US/09/562,919 ; FILING DATE: 02-May-2000 ; CLASSIFICATION: <unknown></unknown>	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFFWARE: Patentin Release #1.0, Version #1.30	; STATE: California; COUNTRY: United States Of America; ZIP: 94104; COMPUTER READABLE FORM:		70 T H III.	; GENERAL INFORMATION: ; APPLICANT: Chamberlain, Jeffrey S. ; Amalfitano, Andrea ; Hauser. Michael A.	; Sequence 1, Application US/09562919 ; Patent No. 645196
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                        CTGCGAGTGTGGCGGTAAACATATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGA 2520
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  CTGCGAGTGTGGCGGTAAACATATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGA
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GENERAL INFORMATION:
APPLICANT: WOLD, William
APPLICANT: TOTH, Karcly
APPLICANT: KUPPASWAMI, Mohan
APPLICANT: LORONIN, KONBANTIN
APPLICANT: DORONIN, KONBANTIN
TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE
TITLE OF INVENTION: REPLICATION-COMPETENT IN TERT-EXPRESSING CELLS
FILE REPERENCE: 16153-8394
CURRENT APPLICATION NUMBER: US/09/956,335
CURRENT APPLICATION NUMBER: US/09/956,335
CURRENT APPLICATION NUMBER: DO1-09-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 35978
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Best Local Similarity 100.0%;
Matches 2594; Conservative 0
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Patent No. 6627190
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ORGANISM: Adenovirus
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GGCGTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGG
                                                                CTGAGATACACCCGGTGGTCCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTG
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                                                                                                                                                                                        CAAGACCTACCCGCCGTCCTAAAATGGCGCCCTGCTATCCTGAGACGCCCGACATCACCTG
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                                                                                                           TGTCTAGAGAATGCAATAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTC
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RESULT 11 US-09-956-335-2 (Sequence 2, Application US/09956335 ; Patent No. 6627190 ; GENERAL INFORMATION: ; APPLICANT: WOLD, William ; APPLICANT: TOTH, Karoly	CATAGAGCAGCTGACCACTTACTGGCTGCAGCCAGGGGATGATTTTGAGGAGGCTATTAG 162
Qy 2581 AGATACAGATTGAG 2594	TTTCAACAGATCAAGGATAATTGCGCTAATGAGCTTGATCTGCTGGCGCAGAAGTATTC 156
Qy 2521 GCTGAGGCCCGATCACTTGGTGCTGGCCTGCACCGCGCTGAGTTTGGCTCTAGCGATGA	AGAGGAGGCTAGGAATCTAGCTTTAGCTTAATGACCAGACACCGTCTGAGTGTATTAC 150
Qy 2461 CTGCGAGTGTGGCGGTAAACATATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGA	1381 TACAGAGGATGGGCAGGGGCTAAAGGGGGTAAAGAGGGAGG
QY 2401 CATGACCATGAAGATCTGGAAGGTGCTGAGGTACGATGAGACCCGCACCAGGTGCAGACC	1321 GGGAATGAATGTTGTACAGGTGGCTGAACTGTATCCAGAACTGAGACGCATTTTGACAAT 1380 
2341 3257	1261 AAGCCAGGCGGCGGCAGGAGCAGAAGCCCATGGAACCCGAGAGCCGGCCTGGACCCTC 1320
	1201 TGTTGTCTTCCGTCCGCCCGGCGATAATACCGACGGAGGAGCAGCAGCAGCAGCAGGAGG 1260
3137	1141 TGGATTTTCTGGCCATGCATCTGTGGGAGAGCGGTTGTGAGACACAAGAATCGCCTGCTAC 1200
2161 CAGGG       3077 CAGGG	1081 TITTGAGTTTTATAAAGGATAAATGGAGCGAAGAAACCCATCTGAGCGGGGGGTACCTGC 1140
2101 CATGO        3017 CATGO	1021 AGAAGGTCATCAAGACTTTTGGATTTTTCCACACCGGGGCGCGCTGCGGGTGCTGTTGCTT 1080
2041 TATCC        2957 TATCC	961 TGAAATCCTGTGGTGAGCTGTTTGATTCTTTGAATCTGGGTCACCAGGCGCTTTTCCAAG 1020 
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2717	721 TGCATGGCGTGTTAAATGGGGCGGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCT 780
1/41 IAGG	661 CGCCTTTGTTTGCTGAATGAAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACT 720
2597 TATCA	601 ACTTGAGCTGTAAACGCCCCAGGCCATAAGGTGTAAACCTGTGATTGCGTGTGTGT
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GAATGTAAGGTTTACTGGCCCCAATTTTAGCGGTACGGTTTTCCTGGCCCAATACCAACCT	GTTACATCTG 792	Ş
2564 TAGATGTAGCATGATAAATATGTGGCCGGGGGTGCTTGGCATGGACGGGTGGTTATTAT 2623	Qy 673 CTGAATGAGTTGAATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACTTGCATGGCGTGT 732	ይ <i>§</i>
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	Qy       313 GTCCTGTGTCTGAACCTGAGCCTGAGCCCAGCCAGAACCCGAGCCTGCAAGACCTACCC 372         Db	<u> </u>
	Qy 253 TTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTTTTAAAAG 312	음 5
TGTACAGGTGGCTGAACTGTATACCACAACTGGAGACCGGCTGTATTTGACAGAGGATGGAT	OY 193 TACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTGGTAATTT 252    - - - - - - - - - - - - - - - - - -	음
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	Qy         13 TGCCACGAGGCTGGCTTTCCACCCAGTGACGAGGAGGATGAGAGGGTGAGGAGTTTGTG         72           Db	р <b>9</b>
AGACTITGGATTTTCCACACCGGGGCGCGCTGCCGCTGCTGTTTTTGACTTTTA	Query Match 99.5%; Score 2582; DB 4; Length 35871; Best Local Similarity 100.0%; Pred. No. 0; Matches 2582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
GTGAGCTGTTTGATTCTTTGAATCTGGGTCACCAGGCGCTTTTCCAAGAGAAAGGTCATCA	LENGTH: 35871 TYPE: DNA ORGANISM: Adenovirus S-09-956-335-2	us ;
913 TAGTCTGCAGAATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTTTGAAATCCTGTG 972	CURRENT FILING DATE: 2001-09-19  NUMBER OF SEQ ID NOS: 3  SOFTWARE: Patentin Ver. 2.0  Db  SEQ ID NO 2	
853 AGAGCTCTAACAGTACCTCTTGGTTTTGGAGGTTTCTGTGGGGCTCATCCCAGGCAAAGT 912	TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE 1 TITLE OF INVENTION: REPLICATION-COMPETENT IN TERT-EXPRESSING CELLS 1 FILE REFERENCE: 16153-8394 1 CURRENT APPLICATION NUMBER: US/09/956,335	
1604 ACCTCATGGAGGCTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGCGTAACTTGCTGGAAC 1663		

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Sequence 4, Application US/08735609

Patent No. 595360

GENERAL INFORMATION:

APPLICANT: Chamberlain, Jeffrey S.
APPLICANT: Amalfitano, Andrea
APPLICANT: Hauser, Michael A.

APPLICANT: Hauser, Michael A.

APPLICANT: Hauser, Michael A.

APPLICANT: Hausers of Connor, Dennis J.

ITITLE OF INVENTION: IMPROVED ADENOVIRUS VE.

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSE: Medlen & Carroll, LLP

STREET: 220 Montgomery Street, Suite 220;

CITY: San Francisco

STATE: California

COUNTRY: United States Of America

ZIP: 94104

COMMITTED PEADABLE FORM.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
OPERATING SYSTEM: PC-DOS,
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ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, biane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: UM-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 2161; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/735,609 FILING DATE:
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TYPE: nucleic acid
STRANDEDNESS: double
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                    AAAGGATAAATGGAGCGAAGAAAACCCATCTGAGCGGGGGGGTACCTGCTGGATTTTCTGGC 1153
                                                               GACTTTGGATTTTTCCACACCGGGGGGCGCTGCTGCTGTTGTTTTTTTGAGTTTTAT 1093
                                                                                                                               TGAGCTGTTTGAATCTTGAATCTGGGTCACCAGGCGCTTTTCCAAAGAGAAGGTCATCAA
                                                                                                                                                    TGAGCTGTTTGATTCTTTGAATCTGGGTCACCAGGCGCTTTTCCAAGAGAAGGTCATCAA 1033
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   AAAGGATAAATGGAGCGAAGAAACCCATCTGAGCGGGGGGTACCTGCTGGATTTTCTGGC
                                                                                                                                                                                              AGTCTGCAGAATTAAGGAGGATTACAAGTGGGGAATTTGAAGAGCTTTTTGAAATCCTGTGG
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ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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	2233 4652	2174 ATGCTGACCTGCTCGGACGGCAACTGTCACCTGCTGAAGACCATTCACGTAGCCAGCC
	2173 4592	2114 AGCGTGGCTGTGATTAAGCATAACATGGTATGTGGCAACTGCGAGGACAGGGCCTCTCAG
	2113	2054 GGTAACTCCAGGGTGCGCCACAATGTGGCCTCCGACTGTGGTTGCTTCATGCTAGTGAAA
	2053	1994 AGCAGGGCTTCAATTAAGAAATGCCTCTTTGAAAGGTGTACCTTGGGTATCCTGTCTGAG
	. 1993 . . 4412	1934 GTAAGGGTTCGGGGCTGTGCCTTTTACTGCTGCTGGAAGGGGGTGGTGTGTCGCCCCAAA
. ~. ~. ~.	1933	1874 ATCCTACACGGTGTAAGCTTCTATGGGTTTAACAATACCTGTGTGGAAGCCTGGACCGAT
	1873	1814 AATGTAAGGTTTACTGGCCCCAATTTTAGCGGTACGGTTTTCCTTGGCCAATACCAACCTT
	1813	1754 AGATGTAGCATGATAAATATGTGGCCGGGGGTGCTTGGCATGGACGGGGTGGTTATTATG
	1753 4172	1694 TGCTACATTTCTGGGAACGGGGCCGAGGTGGAGATAGGATACGGAGGATAGGGTGGCCTTT
7	1693	1634 GTÓGCACTTAGGCCAGATTGCAAGTACAAGATCAGCAAACTTGTAAATATCAGGAATTGT 
RESU US-0 ; Se	1633	1574 ACCACTTACTGGCTGCAGCCAGGGGATGATTTTGAGGAGGCTATTAGGGTATATGCAAAG
Db 43	1573 3992	1514 AAGGATAATTGCGCTAATGAGCTTGATCTGCTGCGCAGAAGTATTCCATAGAGCAGCTG
S B &	1513 3932	1454 AATCTAGCTTTTAGCTTAATGACCAGACACCGTCCTGAGTGTATTACTTTTTCAACAGATC
2 B &	1453 3872	1394 CAGGGGCTAAAGGGGGTAAAGAGGGAGGCGGGGGGCTTGTGAGGCTACAGAGGAGGCTAGG
S B &	3812	1334 GTACAGGTGGCTGAACTGTATCCAGAACTGAGACGCATTTTGACAATTACAGAGGATGGG
S B &	1333 3752	1274 GCGGCAGGAGCAGAGCCCATGGAACCCGAGAGCCGGCCTGGACCCTCGGGAATGAAT
S B &	3692	1214 CCGCCCGGCGATAATACCGACGGAGGAGCAGCAGCAGGAGGAGGAAGCCAGGCGGC
S B 8	1213	1154 CATGCATCTGTGGAGAGCGGTTGTGAGACACAAGAATCGCCTGCTACTGTTGTCTTCCGT

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RESULT 13
US-08-735-609-4
US-08-735-609-4
; Sequence 4, Application US/08735609
; Patent No. 5994132
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Jeffrey S.
; Amalfitano, Andrea
Hauser, Michael A.
;
COMPUTER: PARELE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/735,609
FILING DATE: 23-Oct-1996
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: UM-027
REFERENCE/DOCKET NUMBER: UM-027
REFERENCE/DOCKET NUMBER: UM-02484
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 34303 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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Hartigan-O'Connor, Dennis J.
TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
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ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
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STATE: California
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1274 GCGGCAGGAGCCCATGGAACCCGAGAGCCGGCCTGGACCCTCGGGAATGAAT	1154 CARGCATCTCTGTGAGAGCGGTTGTGAGACAGAAATCGCCTGCTACTGTTCTCTCCGT 1213	34 GACTTTGGATTTTTCCACACCGGGGCGCGCTGCGGCTGCTGTTTTTTTGAGTTTTAT 1	914 AGTCTGCAGAATTAAGGAGGATTACAAGTGGGAATTGAAGAGCTTTTGAAATCCTGTGG 973	94 CCTCATGGAGGCTTGGAAGATTTTCTGCTGGATACTTGCTGGAACA			Query Match Query Match B3.3%; Score 2161; DB 2; Length 34303; Best Local Similarity 100.0%; Pred. No. 0; Best Local Similarity 100.0%; Pred. No. 0; Matches 2161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  434 CAATAGTAGTAGGATAGCTGTGACTCCGGTCCTTCTAACACACCTTCCTGAGATACACCC 493	מ
B	Q & & B	୪ ୫ ୪ ୫ ୪	Q Q dd	0 Db	\$ \$ \$ \$	0 Db	\$\frac{1}{2}\$  \text{Q}  \	
773 CTTGAAGCTCGAGAGCCTGAGGTGAACCTGAACCGGGTGTTTGACATGACCATGAAGGTGACCATGAACCATGAGACCCTGCGAGTGTGGCATGAGACCATGATGAACCATATTAGGAACCCAGCCTGTGATGCTGATGATGACCAGAGAGCATGAGGCCCGATGAAACATATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGAGCAGAGAGCTGAAGGCCCGATGAAACATATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGAGCTGAAGGCCCGATGAAACATATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGAGCTGAAGGCCCGATGAAACATATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGAGCTGAAGGCCCGATGAAACATATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGAGCTGAAGGCCCGATGTAAACATATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGAGCTGAAGGCCCCGATGAGAACATATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGAGCTGAAGGCCCCGATGAGACCATATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGCCCCGATGAGACCATATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGAGCCCCGATGAGACCCAGAGAACATATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGCCCCGATGAGACCATATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGCCCCGATGAGACCATATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGAGCCCGATGAGACCAGAGCCCCGATGAGACCAGAGCCCCGATGAGACCAGAGCCCCGATGAGACCAGAGACCAGACCCAGGCCCGATGAGACCAGACCAGACCAGACCCGATGAGACCCAGAGAGCCCCGATGAGACCAGAGCCCCGATGAGAACATATTAGGAACCAAGCCTGTGAATGCTGGATGTGACCGAGGCCCCGATGAGAGCCCCGATGAGACCAGAGCCCCGATGAGACCAGAGCCCCGATGAGAACATATTAGGAACCAAGCCTGTGAATGTGAACAATATTAGGAACCAAGCCTGAGAGCCTGAGAGCCCGATGAGAACAAAAAAAA	4653 TCTCGCAAGGCCTGGCCAAGGTGTTGAAGCATAACATACTGACCCGCTGTTCCCTTAGATATTG 4712  2294 GGTAACAGGAGGGGGGGTGTTCCTACCTTACCAATGCAATTTGAGTCACACTAAGATATTG 2353	2114 ACCITIGNOTIS IN TANCALISMON TO CONCONCINCUM 21/3 4533 AGCGTGGCTGTGATTAAGCATAACATGGTATGTGGCAAGTGCGAGGACAGGGCCTCTCAG 4592 2174 ATGCTGACCTGCTCGGACGGCAACTGTCACCTTGCTAAGACCATTCACGTAGCCAGCC	AGCAGGGCTTCAATTAAGAAATGCCTCTTTGAAAGGTGTACCTTTGGGTATCCTTCTGAG  13 AGCAGGGCTTCAATTAAGAAATGCCTCTTTGAAAGGTGTACCTTTGGGTATCCTTCTGAG  15 GGTAACTCCAGGGTGCGCACAATGTGGCCTCCGAACTGTGGTTGCTTCATGCTAGTGAAA  1	4293 ATCCTACACGGTGTAAGCTTCTATGGGTTTAACAATACCTGTGTGGAAGCCTGGACCGAT 4352  1934 GTAAGGGTTCGGGGCCTTTTACTGCTGCTGGTAGGGGTGGTGTGTCGCCCCAAA 1993	4173 AGATGTAGCATGATAAATATGTGGCCGGGGGTGCTTGGCATGGACGGGTGGTGATATTATG 4232  1814 AATGTAAGGTTTACTGGCCCCAATTTTAGCGGTACGGTTTTCCTGGCCAATACCAACCTT 1873	4053 ĠTĠĠĊAĊTTĀĠĠĊĊĀĠĀTŢĠĊĀĀĠŤĀĊĀĀĠĀTĊĀĠĊĀĀĀĊŦŢĠŤĀĀĀŤĀŢĊĀĠĠĀĀŦŢĠŤ 4112 1694 ŢĠĊŢĀCĀŢŢŢĊŢĠĠĠĀĀĊŢĠĠĠĠĊĠĀĠĠŢĠĠĀĠĀŢĀĠĠĀŢĀĠ	1454 AATCTAGCTTTTAGCTTAATGACCAGACACCGTCCTGAGTGTATTACTTTTCAACAGATC 1513	

Query Match Bast Local Similarity 100.0%; Pred. No. 0; Matches 2161; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 2161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  434 CAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTGAGATACACCC 493	ATTORNEY/AGENT INFORMATION:  NAME: Ingolia, Diane B,  REGISTRATION NUMBER: 40,027  REFERENCE/DOCKET NUMBER: UM-02484  TELECOMMUNICATION INFORMATION:  TELEPHONE: (415) 705-8410  TELEFAX: (415) 397-8338  INFORMATION FOR SEQ ID NO: 4:  SEQUENCE CHARACTERISTICS:  LENGTH: 34303 base pairs  TYPE: nucleic acid  STRANDEDNESS: double  TOPOLOGY: linear  MOLECULE TYPE: other nucleic acid  DESCRIPTION: /desc = "DNA"  S-09-315-372-4	.ca , Vers	Db 5013 G 5013  RESULT 14  US-09-315-372-4  Sequence 4, Application US/09315372  Patent No. 6057158  GENERAL INFORMATION:  APPLICANT: Chamberlain, Jeffrey S.  APPLICANT: Amalfitano, Andrea  APPLICANT: Hauser, Michael A.  APPLICANT: Hauser, Michael A.  APPLICANT: Hartigan-O'Connor, Dennis J.  TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS  NUMBER OF SEQUENCES: 15  CORRESPONDENCE ADDRESS:  ADDRESSEE: Medlen & Carroll, LLP  STREET: 220 Monteonery Street Suite 2200	–a 2 <u>−</u> 2 ω
	QY 1214 CCGCCCGGCGATAATACCGACGAGGAGCAGCAGCAGCAGGAGGAAGCCAGGCGGC	Oy  974 TGAGCTGTTTGAATCTGGGTCACCAGGCGCTTTTCCAAGAGAAGGTCATCAA 1033	Oy  734 ANATGGGGCGGGGCTTAANGGGTATATAATGCGCCGTGGGCTAATCTTGCATGCATGGCGTGT  Oy  734 ANATGGGGCGGGGCTTAANGGGTATATAATGCGCCGTGGGCTAATCTTGGTTACATCTGA  1	Page 21  y_459_3052.rn1  Page 21  Oy 614 ACGCCCCAGGCCATAAGGTGTAAACCTGTGATTGCGTGTGTTAACGCCTTTGTTTG

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; Sequence 4, Application US/09244752
; Patent No. 6063622
; GENERAL INFORMATION:
APPLICANT: Chamberlain, Jeffrey S
APPLICANT: Amalfitano, Andrea
; APPLICANT: Hauser, Michael A.
; APPLICANT: Kumar-Singh, Rajendra
                                                                                                                            RESULT 15
US-09-244-752-4
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 Chamberlain, Jeffrey Amalfitano, Andrea Hauser, Michael A. Kumar-Singh, Rajendra
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ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane 8.
REGISTRATION NUMBER: 40,027
REGISTRATION POCKET NUMBER: UM-0.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TOTAL POHONE: (415) 705-8410
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 34303 base pairs
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MOLECULE TYPE: other nucleic
DESCRIPTION: /desc = "DNA"
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC com
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TITLE OF INVENTION: IMPROVED ADENOVIRUS VECTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: C
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TYPE: nucleic acid
STRANGENES: double
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CITY: San Francisco
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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   GAGCTCTAACAGTACCTCTTGGTTTTTGGAGGTTTTCTGTGGGGCTCATCCCAGGCAAAGTT
                                                                            CCTCATGGAGGCTTGGGAGTGTTTGGAAGATTTTTTCTGCTGTGCGTAACTTGCTGGAACA 853
                                                                                                                            AAATGGGGGGGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCTTGGTTACATCTGA
                                                                                                                                               AAATGGGGCGGGCTTAAAGGGTATATAATGCGCCCGTGGGCTAATCTTGGTTACATCTGA
                                                                                                                                                                                                    TGAATGAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACTTGCATGGCGTGTT 3152
                                                                                                                                                                                                                       TGAATGAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTTTAACTTTGCATGGCGTGTT
                                                                                                                                                                                                                                                                         GGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGCGTCGCCAGGC
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                                                         CCTCATGGAGGCTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGCGTAACTTGCTGGAACA
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220 Montgomery Street, Suite
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mative 0; Mismatches
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100.0%; Pred. No. 0;
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.99	934 GTAAGGGTTCGGGGCTGTGCCTTTTACTGCTGGAAGGGGGTGGTGTGTCGCCCCAAA
1933 4352	CAATACCTGTGTGGAAGCCTGGACCGAT
1873 4292	814 AATGTAAGGTTTACTGGCCCCAATTTTAGCGGTACGGTTTTCCTGGCCAATACCAACCTT
1813	TGTAGCATGATAAATATGTGGCCGGGGGTGCTTGGCATGGACGGGGTGGTTATTATG
1753 4172	694 TGCTACATTTCTGGGAACGGGGCCGAGGTGGAGATAGATA
1693 4112	634 GTGGCACTTAGGCCAGATTGCAAGTACAAGATCAGCAAACTTGTAAATATCAGGAATTGT 
1633 4052	574 ACCACTTACTGGCTGCAGCCAGGGGATGATTTTGAGGAGGCTATTAGGGTATATGCAAAG
1573 3992	514 AAGGATAATTGCGCTAATGAGCTTGATCTGCTGGCGCAGAAGTATTCCATAGAGCAGCTG
1513 3932	454 AATCTAGCTTTTAGCTTAATGACCAGACACCGTCCTGAGTGTATTACTTTTCAACAGATC
1453 3872	4 CAGGGGCTAAAGGGGGTAAAGAGGGAGCCGGGGGGGCTTGTGAGGCTACAGAGGAGGCTAGG
1393 3812	334 GTACAGGTGGCTGAACTGTATCCAGAACTGAGACGCATTTTGACAATTACAGAGGATGGG
1333 3752	274 GCGGCAGGAGCAGAGCCCATGGAACCCGAGAGCCGGCCTGGACCCTCGGGAATGAAT
1273 3692	214 CCGCCCGGCGATAATACCGACGAGGAGCAGCAGCAGCAGCAGGAGGAAGGA
1213 3632	154 CATGCATCTGTGGAGAGCGGTTGTGAGACACAAGAATCGCCTGCTACTGTTGTCTTCCGT
1153 3572	94 AAAGGATAAATGGAGCGAAGAAACCCATCTGAGCGGGGGTACCTGCTGGATTTTCTGGC
1093 3512	034 GACTTTGGATTTTTCCACACCGGGGGCGCGCTGCGGCTGCTGTTGTTTTTTGAGTTTTTAT
1033	974 TGAGCTGTTTGATTCTTTGAATCTGGGTCACCAGGCGCTTTTCCAAGAGAAAGGTCATCAA
973 3392	ACAAGTGGGAATTTGAAGAGCTTTTGAAATCCTGTGG
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1994 AGCAGGGCTTCAATTAAGAAATGCCTCTTTGAAAGGTGTACCTTGGGTTATCCTGTCTGAG 2053

Search completed: October 31, 2005, 01:17:04 Job time : 438  ${\tt secs}$ 

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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Minimum DB
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Maximum Match 100%
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seq length: 2000000000
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
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(cgm2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
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_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
                                                                      6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
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6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

។«មុខស	Result
1 2594 100.0 3052 2 2594 100.0 7607 3 2594 100.0 7607 4 2594 100.0 7607 5 2594 100.0 7607	Score
1000.0	Query Match Length DB ID
3052 7607 7607 7607 7607	Length
26 10 18	BB
26 US-11-070-890-33 9 US-09-847-101B-34 10 US-09-482-682-48 18 US-10-403-337-41 18 US-10-351-890-41	ID
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## ALIGNMENTS

US-11-070-890-33

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Sequence 33, Application US/11070890
Publication No. US20050170463A1
GENERAL INFORMATION:
APPLICANT: Bout, Abraham
APPLICANT: Opstelten, Jan-Dirk
APPLICANT: Opstelten, Jan-Dirk
TITLE OF INVENTION: RECOMBINANT PROTEIN PRODUCTION IN PERMANENT AMNIOCYTIC CELLS THAT
TITLE OF INVENTION: COMPRISE NUCLEIC ACID ENCODING ADENOVIRUS E1A AND E1B PROTEINS
FILE REFERENCE: 2578-6828US
CURRENT PRILING DATE: 2005-03-04
PRIOR FILLING DATE: 2005-03-04
PRIOR APPLICATION NUMBER: 09/549,463
PRIOR APPLICATION NUMBER: 60/129,452
PRIOR APPLICATION NUMBER: 60/129,452
PRIOR FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.1
SEQ ID NO 33
LENGTH: 3052
TYPE: DNA
ORGANISM: Human Adenovirus Type 5
PEATURE:
OTHER INFORMATION: Nucleotides 459-3510 of Human Adenovirus Type 5
US-11-070-890-33
Query Match
100.0%; Score 2594; DB 26; Length 3052;
Best Local Similarity 100.0%; Pred. No. 0;
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41 GEORGALITICITAMATINATIONAL CONTROLOGICAL MANAGEMENT 120  51 GAGAGATITICITAMATINATIONAL CONTROLOGICAL CONTROLOGICAL STANDARD CONTROLOGI	Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  1 ATCGATCTTACCTGCCACGAGGCTTTCCACCCAGTGACGACGATGAAGAGGGT 60
8 2 8 2 8 2 8 2 8 2 8 2 8 2 8 2 8 2 8 2	ş 8
41 TOGATTTTTCTGGCCCATTCCATCTGTGGACAGGGGTTTTTGGAGACACAAGAATTCGCCTTTCTTAGGATTTTTCTGGGCCATCCAT	1081 TTTTGAGTTTTATAAAGGATAAATGGAGCGAAGAAACCCATCTGAGCGGGGGGGTACCTGC 1140

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Query Match Best Local Similarity 100.0%; Score 2594; DB 9; Length 7607; Best Local Similarity 100.0%; Pred. No. 0; Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy 1 ATCGATCTTACCTGCCACGAGGCTGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGT 60	; SOPTWARE: PatentIn Ver. 2.1 ; SEQ ID NO 34 ; LENGTH; 7607 ; TYPE: DNA ; ORGANISM: Artificial Sequence ; FEATURE: ; OTHER INFORMATION: Description of Artificial Sequence: plasmid GRE5-E1-SV40-Hygro US-09-847-101B-34	; APPLICANT: NEMEROW, GLEN R. ; APPLICANT: FRIEDLANDER, MARTIN ; TITLE OF INVENTION: VECTORS FOR OCULAR TRANSDUCTION AND USE THEREFOR FOR GENETIC THER ; FILE REFERENCE: 22908-1226B ; CURRENT APPLICATION NUMBER: US/09/847,101B ; CURRENT FILLING DATE: 2001-05-01 ; PRIOR APPLICATION NUMBER: 09/562,934 ; PRIOR FILING DATE: 2000-05-01 ; NUMBER OF SEQ ID NOS: 50	RESULT 2 US-09-847-101B-34 IS-equence 34, Application US/09847101B Publication No. US20020193327A1 GENERAL INFORMATION; APPLICANT: VON SEGGERN, DANIEL	Db 2979 GCTGAGGCCCGATCACTTGGTGCTGCACCCCGCGCTGAGTTTGGCTCTAGCGATGA 3038  Qy 2581 AGATACAGATTGAG 2594                Db 3039 AGATACAGATTGAG 3052	2461 CTGCGAGTGTGGCGGTAAACATATTAGGAACCAGCCTGTGATGCTGGACTGACCGAGGA 2	2401 CATGACCATGAAGATCTGGAAGGTGCTGAGGTACGATGAGACCCGCACCAGGTGCAGACC 246	Db 2739 TICCTIGCATITIGGGTAACAGGAGGGGGGGTGTICCTACCTTACCAATGCAATTIGAGTCA 2798  Qy 2341 CACTAAGATATTGCTTGAGCCCGAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTTTGA 2400  Q	Qy 2221 CGTAGCCAGCCACTCTCGCAAGGCCTGGCCAGTGTTTGAGCATAACATACTGACCCGCTG 2280	Qy 2161 CAGGGCTCTCAGATGCTGACCTGCTCGAACGGCAACTGTCACCTGCTGAAGACCATTCA 2220
Q	B & B &		א א א	D Q D	Q D Q	B & 8	\$ \$ B	&	B &
1021 AGAAGGTCATCAAGACTTTGGATTTTCCACACCGGGGCGCGCTGCTGCTGTTGCTT 1080	O1 CCCAGGCAAAGTTAGTCTGCAGAATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTT	81 TGGTTACATCTGACCTCATGAGGCTTGGAGTGTTTGGAAGATTTTTTCTGCTGTGCGTA	661 CGCCTTTGTTTGCTGAATGAGTTGATGAAGATTAAAGGGTGAGATAATGTTTAACT 720	1874 GGCGTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGG 1933  601 ACTTGAGCTGTAAACGCCCCAGGCCATAAGGTGTAAACCTGTGATTGCGTGTGTGT	CTGAGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGATTGGTG	21 TGTCTAGAGAATGCAATAGTAGTAGGATAGCTGTGACTCCGGTCCTTCTAACACACCTC	TITITITAAAAGGTCCTGAACCTGAAGCCTGAGCCAGAACCGGAACCTGAGCCTGAGCCTGAGCCAGAACCGGAACCTGAGCCTGAGCCTGAGACCCGAGACCAGAACCGGAACCTGAGACCTGAGACCTGAGACGCCAGAACACATCACCTGCAAGACCTGAGACGCCCGACATCACCTGCAAGACCTGCTGAGACGCCCGACATCACCTGCAGACGCCTAGACACCTGAGACGCCCGACATCACCTGCAAGACGCCCGACATCACCTGCAAGACGCCCGACATCACCTGACACCTGACACCTGACACCTGACACCACCACCACCACCACCACCACCACCACCACCACCA	241 GTGTGGTAAITTTITITAAITTTITACAGTITITGTGGTTTAAAGAAITTITGTATIGTGA 300	181 GCCATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTTGGGTTTG 240 

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid US-09-482-682-48
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US-09-482-682-48
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APPLICANT: NEMEROW, GLEN R.
APPLICANT: HALLENBECK, FAUL
APPLICANT: STEVENSON, SUSAN
APPLICANT: STRIVENSON, SUSAN
APPLICANT: SKRIPCHENKO, YELENA
APPLICANT: SKRIPCHENKO, YELENA
TITLE OF INVENTION: ADDENOVIRUS VECTORS, PACKAGING CELL LINES, COMPOSITIONS,
TITLE OF INVENTION: AND METHODS FOR PREPARATION AND USE
FILE REFERENCE: 1294.001001
CURRENT APPLICATION NUMBER: US/09/482,682
CURRENT APPLICATION NUMBER: US/09/482,682
CURRENT FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 48
LENGTH: 7607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 48, Application US/09482682 Publication No. US20030157688A1 GENERAL INFORMATION:
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Best Local &
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Sequence 41, Application US/1040337

Publication No. US20030215948A1

GENERAL INFORMATION:
APPLICANT: Kaleko, Michael
APPLICANT: Nemerow, Glen R.
APPLICANT: Smith, Theodore
APPLICANT: Swith, Theodore
APPLICANT: SWITH TOWN TOWNER: Modifications for Efficient Targeting
FILE REFERENCE: 22908-1236B
CURRENT APPLICATION NUMBER: US/10/403,337
CURRENT APPLICATION NUMBER: 10/351,890
PRIOR APPLICATION NUMBER: 60/351,890
PRIOR FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 60/350,388
PRIOR APPLICATION NUMBER: 60/350,388
PRIOR APPLICATION NUMBER: 60/390,967
PRIOR APPLICATION NUMBER: 60/391,967
PRIOR FILING DATE: 2002-06-26

NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin version 3.0

SEQ ID NO 41
LENGTH: 7607
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; FEATURE:
; OTHER INFORMATION: Plasmid GRE5-E1-SV40-Hygro
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RESULT 5 US-10-351-890-41 ; Sequence 41, Application US/10351890

음 성 음

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APPLICANT: Kaleko, Michael
APPLICANT: Kaleko, Michael
APPLICANT: Kaleko, Michael
APPLICANT: Smith, Theodore
APPLICANT: Smith, Theodore
ITITLE OF INVENTION: Fiber Shaft Modifications for
FILE REFERENCE: 22908-1236
CURRENT APPLICATION UNMBER: US/10/351,890
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: 60/350,388
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: 60/391,967
PRIOR FILING DATE: 2002-06-26
INUMBER OF SEQ ID NOS: 72
SOFTMARE: Patentin version 3.0
SEQ ID NO 41
LENGTH: 7607
TYPE: DNA
COCAMICAN: Artificial Sequence
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OTHER INFORMATION: Plasmid GRE5-E1-SV40-Hygro US-10-351-890-41
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Best Local Similarity
Matches 2594; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Publication No. US20040002060A1 GENERAL INFORMATION:
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CGCCTTTGTTTGCTGAATGAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACT 720
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                              TGTCTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTC
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1561 CATAGAGCAGCTGACCACTTACTGGCTGCAGCCAGGGGATGATTTTGAGGAGGCTATTAG 1620	4 4 4 4 4	TETTGTCTTCCGTCCCCCGGCGATAATACCGACGAGGAGGAGCAGCAGCAGCAGCAGGAGGAGGAGG	1021 AGAAGTCATCAAGACTITGGATTCTTTGAATCTGGGTCACCAGGGGCTTTCCAAG 2353  1021 AGAAGGTCATCAAGACTITGGATTTTTCCACACCGGGGCGGGG	ACTTGCTGGAACAGAGCTCTAACAGTACCTCTTGGTTTTTGGAGGTTTCTGTGGGGCTCAT	
RESULT 6 US-10-731-961-3 ; Sequence 3, Application US/10731961 ; Publication No. US20050130306A1 ; Publication No. US20050130306A1 ; GENERAL INFORMATION: ; TITLE OF INVENTION: VIRAL VECTORS WHOSE REPLICATION AND, OPTIONALLY, PASSENGER GENE ; TITLE OF INVENTION: ARE CONTROLLED BY A GENE SWITCH ACTIVATED BY HEAT IN THE PRESENCE ; TITLE OF INVENTION: OR ABSENCE OF A SMALL MOLECULE REGULATOR ; FILE REFERENCE: Replicating virus ; CURRENT APPLICATION NUMBER: US/10/731,961 ; CURRENT FILING DATE: 2003-12-10 ; PRIOR APPLICATION NUMBER: 09/939,161 ; PRIOR FILING DATE: 2001-08-24	Qy 2461 CTGCGAGTGTGGCGGTAAACATATTAGGAACCAGCCTGTCATGCTGCATGTCACCGAGGA 2520	OY 2281 TICCTTGCATTIGGGTAACAGGAGGGGGGTGTTCCTACCTTACCAATGCAATTTGAGTCA 2340	Qy 2101 CATGCTAGTGAAAAGCGTGGCTGTGATTAAGCATTAACATGGTATGTGGCAACTGCGAGGA 2160	Oy  1921 AGCCTGGACCGATGTAAGGGTTCGGGGCTGTGCCTTTTACTGCTGCTGGAAGGGGGTGGT 1980	Db 3074 TAGGGTGGCCTTTAGATGTAGCATGATAAATATGTGGCCGGGGGTGCTTGGCATGGACGG 3133  Qy 1801 GGTGGTTATTATGAATGTAAGGTTTACTGGCCCCAATTTTAGCGGTACGGTTTTCCTGGC 1860

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2776 CAATACCAACCTTATCCTACACGGTGTAAGCTTCTATGGGTTTAACAATACCTGTGTGGA	Oy 781 TGGTTACATCTCACCTCATGGAGGCTTGGGAGGTTTTTGGAAGATTTTTCTGCTGTGCGTA 840 Db 1696 TGGTTACATCTGACCTCATGGAGGCTTGGGAGTTTTTGGAAGATTTTTCTGCTGTTACATCTGATGGAGGCTTGGGAGTTTTTGGAAGATTTTTCTGCTGTTACATCTGATGGAGGCTTGGGAAGATTTTTCTGCTTTTTTTT
1861 CAATACCAACCTTATCCTACACGGTGTAAGCTTCTATGGGTTTTAACAATACCTGTGTGGA	TGCATGGCGTGTTAAATGGGGCGTGGGCTAAATGT
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2476 CATAGAGCAGCTGACCATTACTGGCTGCAGGCGATGATTTTGAGGAGGCTATTAG	Qy 481 CTGAGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTG 540
1501 ITTTCAACAGATCAAGGATAATIGCGCTAATGAGCTTGATCTGCTGGCGCAGAAGTATIC	Qy         421         TGTCTAGAGAATAGTAGTAGTAGGATAGCTGTGACTCCGGTCCTTCTAACACACCTC         480
2356 AGAGGAGCTAGGATCTAGCTTTAGCTTAATGACCAGACACCGTCCTGAGTGTATTAC	Qy         361         CAAGACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTG         420
121 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	OY 301 TITTITAAAAGGTCCTGAGCCTGAGCCTGAGCCCGAGCCAGAACCTG 360
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1321 AGGLAGGUGGUGGUGGAGAGCAGAAGCCCATGGAACCGGAGAGCAGAACCCTGGACCCTC  1321 AGGCCAGGCGGCGGCAGGAGCAGAAGCCCATGGAACCCGAGAGCCGGACCCTGGACCCCTC  1321 AGGCAATGAATGAACCGGCGGCGGAGCAGAGCCGACCCTCCTC	Qy 181 GGCATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTTGG 240
121 ISTICITICOSTCOSCOSCISATANTACISACISASSAGCASCASCAGCAGCAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGG	Qy         121 CACCGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTTGCTATATGAGGACCTGT 180         CACCGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTTGCTATATGAGGACCTGT 180         CACCGGAGGAATACGGGGGGACCCAGATATTATGTTGTTCGCTTTTGCTATATGAGGACCTGT 1095         CACCGGAGGAATACGGGGGGACCCAGATATTATGTTGTTCGCTTTTGCTTATATGTTGTTGTTTTGCTTATATGTTGTTTTTTTT
111 IGGATITICIGGCATGCATCTGTGGAGAGCGGTTGTGAGACACAAGAATCGCCTGCTAC	Qy 61 GAGGAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTAT 120   Db 976 GAGGAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTAT 1035
1001 III ISAS II IIA IAMASAI IAMA ISSANCUSAAANCUCAICIGAS COGAGGIACCIGC	Qy         1 ATCGATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGACGAGGATGAAGAGGGT 60         Qy         1
1021 KGARGGTCATCARGACTTTGGATTTTTCCRACCGGGGGGGGCGGCTGCTGGTTGCTTT	core 2594; DB 24; Length 9905; red. No. 0; Mismatches 0; Indels 0; Gaps 0;
961 TGAAATCCTGTGGTGAGCTGTTTGATTCTTTGAATCTGGGTCACCAGGCGCTTTTCCAAG	; ORGANISM: Artificial Qy; PEATURE: ; PEATURE: ; OTHER INFORMATION: pxcl plasmid pb US-10-731-961-3
901 CCCAGGCAAAGTTAGTCTGCAGAATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTT 960 	SOFTWARE: PatentIn version 3.3  SEQ ID NO 3  LENGTH: 9905  Db  TYPE: DNA
	PRIOR APPLICATION NUMBER: 60/191,580  PRIOR FILING DATE: 2000-03-23  NUMBER OF SEO ID NOS: 4  Db

2845 AGAAGGTCATCAAGACTTTGGATTTTCCACACCGGGGCGCGCTGCGGCTGCTGTTGCTT 2904	ם א עץ	Query Match 100.0%; Score 2594; DB 9; Length 11152; Best Local Similarity 100.0%; Pred. No. 0;
IGAAATICCTGTGGTGAGCTGTTTGATTCTTTGATTCTGGGTCACCAGGCGCTTTTCCAAG	) B &	; OKGANISH: ATTITICIAL Sequence; ; FEATURE: ; OTHER INFORMATION: Description of Artificial Sequence: plasmid US-09-847-101B-12
CCAGGCAAAGTTAGTCTGCAGAATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTT	p &	SEQ ID NO 12  LENGTH: 11152  TYPE: DNA
ACTTGCTGGAACAGAGCTCTAACAGTACCTCTTGGTTTTGGAGGTTTCTGTGGGGCTCAT 9	עם פט	LING DATE: 2001-0 ICATION NUMBER: 0: NG DATE: 2000-05-0 SEQ ID NOS: 50
781 TGGTTACATCTGACCTCATGGAGGCTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGCGTA 840	ТНВЯ ОУ ОУ	APPLICANT: FRIEDLANDER, MARTIN TITLE OF INVENTION: VECTORS FOR OCULAR TRANSDUCTION AND USE THEREFOR FOR GENETIC FILE REFERENCE: 22908-1226B CURRENT APPLICATION NUMBER: US/09/847,101B
721 TGCATGGCGTGTTAAATGGGGCGGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCT 780 	Db 97	PUBLICATION NO. US20020193327A1 ; PUBLICATION NO. US20020193327A1 ; GENERAL INFORMATION: ; APPLICANT: VON SEGSERN, DANIEL ; APPLICANT: NEMEROW, GLEN R.
661 CGCCTTTGTTTGCTGAATGAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACT 720	Qy	RESULT 7 US-09-847-101B-12 . Semiesne 12 Application US/00847101B
601 ACTTGAGCTGTAAACGCCCCAGGCCATAAGGTGTAAACCTGTGATTGCGTGTGTGT	Qy	Qy 2581 AGATACAGATTGAG 2594
541 GGCGTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGG 600	Qy	Qy 2521 GCTGAGGCCCGATCACTTGGTGCTGGCCTGCACCCGCGCTGAGTTTGGCTCTAGCGATGA 2580
481 CTGAGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTG 540	Qy Db	Qy 2461 CTGCGAGTGTGGCGGTAAACATATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGA 2520
421 TGTCTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCCTC 480	Qy dg	Qy 2401 CATGACCATGAAGATCTGGAAGGTGCTGAGGTACGATGAGACCCGCACCAGGTGCAGACC 2460
361 CAAGACCTACCGGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTG 420	Qy	Qy 2341 CACTAAGATATTGCTTGAGCCCGAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTTTGA 2400
301 TITITITAAAAGGICCTGIGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTG 360 	Qy	Qy 2281 TTCCTTGCATTTGGGTAACAGGAGGGGGTGTTCCTACCTTACCAATGCAATTTGAGTCA 2340
241 GIGIGGTAATTTITTTTAATTTITACAGITTIGGGTTTAAAGAATTTIGTATIGTGA 300 	Qy Db	Qy 2221 CGTAGCCAGCCACTCTCGCAAGGCCTGGCCAGTGTTTTGAGCATACATA
181 GGCATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTG 240	Qy Db	Qy 2161 CAGGGCCTCTCAGATGCTGACCTGCTCGGACGCAACTGTCACCTGCTGAAGACCATTCA 2220
121 CACCGGAGGAATACGGGGGACCCAGATATTATGTGTTTCGCTTTGCTATATGAGGACCTGT 180	dg Vo	Qy 2101 CATGCTAGTGAAAAGCGTGGCTGTGATTAAGCATAACATGGTATGTGGCAACTGCGAGGA 2160
61 GAGGAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTAT 120	Qy	Qy 2041 TATCCTGTCTGAGGGTAACTCCAGGGTGCGCCACAATGTGGCCTCCGACTGTGGTTGCTT 2100
1 ATCGATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGAGGATGAAGAGGGT 60	Qy	Qy 1981 GTGTCGCCCCAAAAGCAGGGCTTCAATTAAGAAATGCCTCTTTGAAAGGTGTACCTTGGG 2040
Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	мат	Db 2836 AGCCTGGACCGATGTAAGGGTTCGGGGCTGTGCCTTTTACTGCTGCTGGAAGGGGGTGGT 2895

160	2101 CATGCTAGTGAAAAGCGTGGCTGTGATTAAGCATAACATGGTATGTGGCAACTGCGAGGA 2
100	2041 TATCCTGTCTGAGGGTAACTCCAGGGTGCGCCACAATGTGGCCTCCGACTGTGGTTGCTT 2
040	981 GTGTCGCCCCAAAAGCAGGCTTCAATTAAGAAATGCCTCTTTGAAAGGTGTACCTTGGG 2 
980	CTGGACCGATGTAAGGGTTCGGGGCTGTGCCTTTTACTGCTGCTGGAAGGGGGTGGT 1 
920	₽ <u>—</u> ₽
860	766C 1
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740	681 TATCAGGAATTGTTGCTACATTTCTGGGAACGGGGCCGAGGTGGAGATAGAT
504	621 GGTATATGCAAAGGTGGCACTTAGGCCAGATTGCAAGTACAAGATCAGCAAACTTGTAAA 1
620	561 CATAGAGCAGCTGACCACTTACTGGCTGCAGCCAGGGGATGATTTTGAGGAGGCTATTAG 1
560 384	501 TTŤTCAACAGATCAAGGATAATTGCGCTAATGAGCTTGATCTGCTGGCGCAGAAGTATTC 1
324	1441 AGAGGAGGCTAGGAATCTAGCTTTTAGCTTAATGACCAGACACCGTCCTGAGTGTATTAC 1
440 264	381 TACAGAGGATGGGCAGGGGCTAAAGGGGGTAAAGAGGGAGCCGGGGGGGG
380	TGAATGTTGTACAGGTGGCTGAACTGTATCCAGAACTGAGACGCATTTTGACAAT 1 
320	NACCCGAGAGCCGGCCTGGACCCTC 1
260	1201 TGTTGTCTTCCGTCCGCCCGGCGATAATACCGACGAGGAGCAGCAGCAGCAGCAGCAGGAGG 1
200	1141 TGGATTTTCTGGCCATGCATCTGTGGAGAGGGGTTGTGAGACACAAGAATCGCCTGCTAC 1
140	081 TTTTGAGTTTTATAAAGGATAAATGGAGCGAAGAAACCCATCTGAGCGGGGGGTACCTGC 1

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GENERAL INFORMATION:

APPLICANT: VON SEGGERN, DANIEL
APPLICANT: NEMEROW, GLEN R.

APPLICANT: HALLENBECK, PAUL
APPLICANT: STRYENSON, SUSAN
APPLICANT: SKRIPCHENKO, YELENA
APPLICANT: SAPENOVIRUS VECTORS, PACKAGING CELL LINES, COMPOSITIONS,
TITLE OF INVENTION: AND METHODS FOR PREPARATION AND USE
FILE REFERENCE: 1294.0010001
CURRENT APPLICATION NUMBER: US/09/482,682
CURRENT FILING DATE: 2000-01-14
SOFTWARE: PATENTION: NEGRETATION AND USE
FEATURE: US/09/482,682
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE: TYPES TYPES THEODERICATION NEGRETATION OF SECULATION OF
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US-09-482-682-12
US-09-482-682-12
; Sequence 12, Application US/09482682
; Publication No. US20030157688A1
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2594; Conservative 0; Mismatches
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                                                                                                                                                              61 GAGGAGTTTGTGTTAGATTATGTGGAGCACCCCCGGGCACGGTTGCCAGGTCTTGTCATTAT 120
                                                                                                                                                                                                                                                                                         1 ATCGATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGT
CACCGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGT 180
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1081 TTTTGAGTTTTATAAAGGATAAATGGAGCGAAGAAACCCATCTGAGCGGGGGGGTACCTGC 1140	901 CCCAGGCAAAGTTAAGTCTGCAGAATTAAAGAGGATTACAAAGTGGGAATTTGAAGAGCTTT 960	721 TGCATGGCGTGTTAAATGGGGCGGGCTTAAAGGGTATATAATGCGCCCGTGGGCTAATCT 780		CCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACA	GGCATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTG
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2341 CACTAAGATATTTGCTTGAGCCCGAGAGCATGTCCAAGGTGAACCTGCAACGGGGTGTTTGA 2231 CACTAAGATTTTGAGCCAGAGGCCAGTGTTCCAAGGTCAACATTCAACATTCAACATTCAACATTCAACATTCAACATTCAACATTCAACATTCAACATTCAACATTCAACATTCAACATTCAACATTCAACATTCAACATTCAACATTCAACATTCAACATTCAACCATTCAACATTCAACATTCAACCATTCAACATTCAACCATTCAACCATTCAACCATTCAACCATTCAACCATTCAACCATTCAACCATTCAACCATTCAACCATTCAACCATTCAACCATTCAACCATTCAACCATTCAACATTCAACCATTCAACCATTCAACCATTCAACATTCAACATTCAACATTCAACATTCAACCATTCAATTCAACATTCAACATTCAACATTCAACATTCAACATTCAACATTCAACATTCAACATTCAACACAACA	81 GTGTCGCCCCAAAAGCAGGCTTCAATTAAGAAATGCCTCTTTGAAAGGTGTACCTTGGG	GTTGTTATTATGAATGTAAGGTTTACTGGCCCCAATTTTAGCGGTACGGTTTTCCTGGC CAATACCAACCTTATCCTACACGGTGTAAGCTTCTATGGGTTTTAACAATACCTGTGTGGA	3445 ĠĠTĀTĀTĠĊĀĀĀĠĠĠĠĊĀCŤTĀĠĠĊĊĀĠĀTĠĊĀĠĀTĊĀĠĀTĊĀĠĀĀĀĊŦĠŢĀĀĀ 3504  1681 TATCAGGAATTGTTGCTACATTTCTGGGAACGGGCCGAGGTGGAGATĀGATĀGĀGĀT		1261 AAGCCAGGCGGCGGCAGGAGCAGAGCCCATGGAACCCGAGAGCCCGGCCTGGACCCTC 1320

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361	QY 301 TTTTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTG	Qy 241 GTGTGGTAATTTTTTTTTTAATTTTTTACAGTTTTGTGGTTTAAAGAATTTTGTAATTGTGA	OY 181 GCATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGGTTTG	QY 121 CACCGGAGGAATACGGGGGACCCAGATATTATGTGTTTCGCTATATGAGGACCTGT	Qy 61 GAGGAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTAT	GGCTGGCTTTCCACCCAGTGA               GGCTGGCTTTCCACCCAGTGA	Query Match 100.0%; Score 2594; DB 9; Length 14455 Best Local Similarity 100.0%; Pred. No. 0; Matches 2594; Conservative 0; Mismatches 0; Indels 0;	ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Description of Artificial Sequence: 'S-09-847-101B-15	; SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 15 ; LENGTH: 14455 ; TYPE: DNA	; CURRENT FILING DATE: 2001-05-01 ; PRIOR APPLICATION NUMBER: 09/562,934 ; PRIOR FILING DATE: 2000-05-01 ; NUMBER OF SEQ. ID NOS: 50	APPLICANT: FRIEDLANDER, MARTIN ITTLE OF INVENTION: VECTORS FOR OCULAR TRANSDUCTION AND USE FILE REFERENCE: 22908-1226B CURRENT APPLICATION NUMBER: US/09/847.101B	Publication No. US20020193327A1  GENERAL INFORMATION: APPLICANT: VOM SEGGERN, DANIEL APPLICANT: NEMEROW. GIEN R	RESULT 9 US-09-847-101B-15 ; Sequence 15. Application US/09847101B	Qy 2581 AGATACAGATTGAG 2594	Qy 2521 GCTGAGGCCCGATCACTTGGTGCTGGCCTGCACCCGCGCTGAGTTTGGCTCTAGCGATGA	Qy 2461 CTGCGAGTGTGGCGGTAAACATATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGA	Qy 2401 CATGACCATGAAGATCTGGAAGGTGCTGAGGTACGATGAGACCCGCACCAGGTGCAGACC	Db 4165 CACTAAGATATTGCTTGAGCCCGAGAGCATGTCCAAGGTGAACCTGAACGGGGTGTTTGA
	Oy	300	240	180		60 18	0; Gaps 0; Db	plasmid Oy	Oy Ob	Qy Qy	USE THEREFOR FOR GENETIC THER Db	Oy Oy	Оу	Db Qy	CTCTAGCGATGA 2580 Qy              CTCTAGCGATGA 4404 Db	CTGGATGTGACCGAGGA 2520 OY 	CCAGGTGCAGÀCC 2460              CAGGTGCAGÀCC 4284 Db	
1441 AGAGGAGGCTAGGAATCTAGCTTTAGCTTAATGACCAGACACCGTCCTGAGTGTATTAC 1500	1381 TACKGA/GATGGCAGGGGTAAAGGGGGTAAAGAGGAGGGGGGGGGTTGTGAGGCTAC 1440	GGAATIGAATGTTGTTACAGGTGGCTGAACTGTATCCAGAACTCAGACGCATTTTGACAAT	ANGCCAGGCGGCGGCAGGAGGCAGAGCCCATGGAACCCGAGAGCCGGCCTGGACCCTC	TGTTGTCTTCCGTCCGCCGGCGATAATACCGACGGAGGAGCAGCAGCAGCAGCAGCAGGAGGAGGAG	1141 TGGATTTTCTGGCCATGCATCTGTGGAGAGGGGTTGTGAGACACAAGAATCGCCTGCTAC 1200	1081 TTTTGAGTTTTATAAAGGATAAATGGAGCGAAGAAACCCATCTGAGCGGGGGTACCTGC 1140 	1021 AGAAGGTCATCAAGACTTTGGATTTTTCCACACCGGGGCGCGCTGCGGCTGCTGTTGCTT 1080	961 TGAAAICCTGTGGTGAGCTGTTTGATTCTTTGAATCTGGGTCACCAGGCGCTTTTCCAAG 1020 	901 CCCAGGCAAAGTTAGTCTGCAGAATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTT 960 	841 ACTIGCTGGAACAGAGCTCTAACAGTACCTCTTGGTTTTGGAGGTTTCTGTGGGGGCTCAT 900	781 TGGTTACATCTGACCTCATGGAGGCTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGCGTA 840	721 TGCATGGCGTGTTAAATGGGGCGGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCT 780 	661 CGCCTTTGTTTGCTGAATGAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACT 720 	601 ACTTGAGCTGTAAACGCCCCAGGCCATAAGGTGTAAACCTGTGATTGCGTGTGTGGGTTAA 660	541 GGCGTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGG 600	481 CTGAGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTG 540	421 TGTCTAGAGAATGCAATAGTAGTAGGATAGCTGTGACTCCGGTCCTTCTAACACACCCTC 480	

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Sequence 15, Application US/09482682

Publication No. US20030157688A1

GENERAL INFORMATION:

APPLICANT: VON SEGGERN, DANIEL

APPLICANT: NEMEROW, GLEN R.

APPLICANT: HALLENBECK, PAUL

APPLICANT: SKRIPCHENKO, YELENA

TITLE OF INVENTION: AND METHODS FOR PREPARATION AND USE

FILE REFERENCE: 1294.001001

CURRENT APPLICATION NUMBER: US/09/482,682

CURRENT APPLICATION UNUMBER: US/09/482,682

CURRENT FILING DATE: 2000-01-14

NUMBER OF SEQ ID NOS: 76

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 15

LENGTH: 14455

TYPE: DNA

ORGANISM: Artificial Sequence
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Best Local Similarity 100.0%; Pred. No. 0;
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                GGCGTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGG
                                                                 CTGAGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTTGGTG
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; FUDILICACION NO. USZOUPOZOZOSAI ; GENERAL INFORMATION: ; APPLICANT: Shanghai Sunway Biotech Co., LTD. ; TITLE OF INVENTION: Treatment for Metastatic Cancer	1621 GGTATATGCAAAGGTGGCACTTAGGCCAGATTGCAAGTACAAGATCAGCAAACTTGTAAA 1680 
RESULT 11 US-10-766-307A-3 US-10-766-307A-3 ; Sequence 3, Application US/10766307A	1561 CATAGAGCAGCTGACCACTTACTGGCTGCAGCCAGGGGATGATTTTGAGGAGGCTATTAG 1620
QY 2581 AGATRCAGATTGAG 2594	1501 TTTTCAACAGATCAAGGATAATTGCGCTAATGAGCTTGATCTGCTGGCGCAGAAGTATTC 1560
2521 GCTGAGGCCCGATC	1441 AGAGGAGGCTAGGAATCTAGCTTTAGCTTAATGACCAGACACCGTCCTGAGTGTATTAC 1500
2461 CIGCGAGIGIGGGGGTAAACATATTAGGAACCAGCCIGIGATGCIGGATGTGACCGAGGA	1381 TACAGAGGATGGGCAGGGGCTAAAGGGGGTAAAGAGGGAGCCGGGGGGCTTGTGAGGCTAC 1440
2401 CATGACCATGAAGATCTGGAAGGTGCTGAGGTACGATGACCCGCACCAGGTGCAGACC	1321 GGGAATGAATGTTGTACAGGTGGCTGAACTGTATCCAGAACTGAGACGCATTTTGACAAT 1380
2341 CACTAAGATATTGCTTGAGCCCGAGAGCAGGTGAACCTGAACGGGGTGTTTGA	1261 AAGCCAGGCGGCGGCAGGAGCAGAAGCCCATGGAACCCGAGAGCCGGCCTGGACCCTC 1320
4105 TICCTIGCATTIGGGTAACAGGAGGGGGGTTCCTACCTTACCAATGCAATTIGAGTCA	1201 TGTTGTCTTCCGTCCGCCGGCGATAATACCGACGGAGGAGCAGCAGCAGCAGCAGCAGGAGG 1260
2221 CSTAGCCACTCTCGCAAGGCTGGCCAGTGTTTGAGCATAACATACTGACCGCTG 4045 CGTAGCCACTCTCGCAAGGCCTGGCCAGTGTTTGAGCATAACATACTGACCGCTG	1141 TGGATTTTCTGGCCATGCATGTGTGGAGAGAGCGGTTGTGAGACACAAGAATCGCCTGCTAC 1200
2181 CAGGGCCTCTCAGATGCTGACCTGCTCGGACGGCAACTGTCACCTGCTGAAGACCATTCA 3985 CAGGGCCTCTCAGATGCTGACCTGCTCGGACGGCAACTGTCACCTGCTGAAGACCATTCA 3985 CAGGGCCTCTCAGATGCTGACCTGCTCGGACGGCAACTGTCACCTGCTGAAGACCATTCA	1081 TTTTGAGTTTTATAAAGGATAAATGGAGCGAAGAAAACCCATCTGAGCGGGGGGTACCTGC 1140
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201 TATICCIGITCIGAGGGTAACTICCAGGGTGCCCACAATGIGGCCTCCGACTGTGGTTGCTT	961 TGAAATCCTGTGGTGAGCTGTTTGAATCTTTGAATCTGGGTCACCAGGCGCTTTTCCAAG 1020
1981 GIGICGCCCCAAAAGCAGGGCTICAATTAAGAAAIGCCTCTITIGAAAGGIGTACCTTIGGGTIGTAAAGGIGTACCTTIGGGTIGTAAAGGIGTACCTTIGGGTIGTAAAGGIGTAACCTTIGGGTIGTAAAGGIGTAACCTTIGGGTIGTAAAGGIGTAACCTTIGGGTIGTAAAGGIGTAACCTTIGGGTIGTAAAGGIGTAACCTTIGGGTIGTAAAGGIGTAACCTTIGGGTIGTAAAGGIGTAACCTTIGTAAAGGIGTAACCTTIGTAAAGGIAAAGGIAAAGGIAAAGGIAAAGGIAAAGGIAAAAGGIAAAGGIAAAGGIAAAGGIAAAGGIAAAGGIAAAGGIAAAGGIAAAGGIAAAGGIAAAGGIAAAAGGIAAAAGGIAAAAGGIAAAAGGIAAAAGGIAAAAGGIAAAAGGIAAAAGGIAAAAAGGIAAAAAGGIAAAAAGGIAAAAAA	901 CCCAGGCAAAGTTAGTCTGCAGAATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTT 960
1921 AGCCTGGACCGATGTAAGGGTTCGGGGCTGTTTACTGCTGCTAGAAGGGGTTGGT	841 ACTTGCTGGAACAGAGCTCTAACAGTACCTCTTGGTTTTTGGAGGTTTCTGTGGGGGCTCAT 900
1881 CAMIACCANCCITATCCIRCACGGIGIAGGITTCIAIGGGITTAACAAIACCIGIGIGGA	781 TGGTTACATCTGACCTCATGGAGGCTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGCGTA 840
1861 GAARAGGAAAGGTTAAGGGTAAGGGTTACTGGCCCAATTTTAGGGGTACGGTTTTCCTGGC	721 TGCATGGCGTGTTAAATGGGGCGGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCT 780 
1911 INGGGTGGCCTTTNGATGTNGCATGATAATATGTGGCCGGGGGTGCTTGGCATGGACGG 3565 TAGGGTGGCCTTTAGATGTNGCATGATAATATGTGGCCGGGGGTGCTTGGCATGGACGG	661 CGCCTTTGTTTGCTGAATGAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACT 720 
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; FILE REFERENCE: 121300.00003
; CURRENT APPLICATION NUMBER: US/10/766,307A
; CURRENT FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 32802
; TYPE: DNA
; ORGANISM: Adenovirus
US-10-766-307A-3
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Sequence 43, Application US/09725720

Patent No. US20010049136A1

GENERAL INFORMATION:
APPLICANT: IMLER, Jean-Luc
APPLICANT: IMLER, Jean-Luc
APPLICANT: MEHTALI, Majid
APPLICATION: COMPLEMENTATION LINES
NUMBER OF SEQUENCES: 43
COMPLENCES AND CORRESPONDING
INTEET: 1737 King Street, Swecker & MATHIS, L.L.P.
STREET: 1737 King Street, Swite 500
STATE: Virginia
COUNTRY: United States
INTER: Virginia
COMPUTER: Nataballe FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pacentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION MEMBER. MIS /00/775 720
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FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Dadio, Susan M.
REGISTRATION NUMBER: 40,373
REFERENCE/DOCKET NUMBER: 0293
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 2594; Conserv
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APPLICATION NUMBER:
FILING DATE:
PRIOR APPLICATION DATA:
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TGCATGGCGTGTTAAATGGGGCGGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCT
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                                                                                             CGCCTTTGTTTGCTGAATGAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACT
                                                                                                                                                       ACTTGAGCTGTAAACGCCCCAGGCCATAAGGTGTAAACCTGTGATTGCGTGTGTTGATTAA
                                                                                                                                                                                                         GGCGTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGG
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SEQ ID NO 4 LENGTH: 35935	1801 GGTGGTTATTATGAATGTAA3GTTTACTGGCCCCAATTTTAGCGGTACGGTTTTCCTGGC 1860 
CURRENT FILING DATE FRIOR APPLICATION FRIOR FILING DATE: FRIOR FILING	1741 TAGGGTGGCCTTTAGATGTAGCATGATAAATATGTGGCCGGGGGTGCTTGGCATGGACGG 1800
APPLICANT: GRACES FITTLE OF INVENTION FILE REFERENCE: ST	1681 TATCAGGAATTGTTGCTACATTTCTGGGAACGGGGCCGAGGTGGAGATAGAT
	1621 GGTATATGCAAAGGTGGCACTTAGGCCAGATTGCAAGTACAAGATCAGCAAACTTGTAAA 1680 
RESULT 13 US-09-782-378A-4 ; Sequence 4 Applica	1561 CATAGAGCAGCTGACCACTTACTGGCTGCAGCCAGGGGATGATTTTGAGGAGGCTATTAG 1620
Db 3497 AGATACA	1501 TITTCAACAGATCAAGGATAATTGCGCTAATGAGCTTGATCTGCTGGCGCAGAAGTATTC 1560 
3437	1441 AGAGGAGGCTAGGAATCTAGCTTTTAGCTTAATGACCAGACACCGTCCTGAGTGTATTAC 1500 
	1381 TACAGAGGATGGGCAGGGGCTAAAGGGGGTTAAAGAGGGAGCCGGGGGCTTGTGAGGCTAC 1440
	1321 GGGAATGATGTTGTACAGGTGGCTGAACTGTATCCAGAACTGAGACGCATTTTGACAAT 1380 
3257	1261 AAGCCAGGCGGCGGCAGGAGCAGAGCCCATGGAACCCGAGAGCCGGCCTGGACCCTC 1320
3197	1201 TGTTGTCTTCCGTCCGCCCGGCGATAATACCGACGAGGAGCAGCAGCAGCAGCAGCAGGAGGAGGAGCAGC
3137	1141 TGGATTTTCTGGCCATGCATCTGTGGAGAGCCGGTTGTGAGACAACAAGAATCGCCTGCTAC 1200
3077	1081 TTTTGAGTTTTATAAAGGATAAATGGAGCGAAGAAACCCATCTGAGCGGGGGGGTACCTGC 1140
3017	1021 AGAAGGTCATCAAGACTTTTGGATTTTTCCACACCGGGGCGCGCTGCGGCTGCTGTTGCTT 1080
2957	961 TGANATCCTGTGGTGAGCTGTTTGATTCTTTGAATCTGGGTCACCAGGCGCTTTTCCAAG 1020 
2897	901 CCCAGGCAAAGTTAGTCTGCAGAATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTT 960 
2837	841 ACTTGCTGGAACAGAGCTCTAACAGTACCTCTTGGTTTTTGGAGGTTTCTGTGGGGCTCAT 900
2777	781 TGGTTACATCTGACCTCATGGAGGCTTGGGAGTGTTTGGAAGATTTTTCTGCTGTGCGTA 840
Oy 1861 CAATACC	1637 TGCATGGCGTGTTAAATGGGGCGGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCT 1696

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                             GCCCGATCACTTGGTGCTGGCCTGCACCCGCGCTGAGTTTGGCTCTAGCGATGA
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AGATTGAG 3510
                                     GCCCGATCACTTGGTGCTGGCCTGCACCCGCGCTGAGTTTGGCTCTAGCGATGA
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US-09-782-378A-4

Sequence 4, Application US/09782378A

Patent NO. US20020102731A1

GENERAL INFORMATION:
APPLICANT: Hearing, Patrick
APPLICANT: Bahou, Wadie
APPLICANT: Sandalon, Ziv
APPLICANT: Gnatenko, Dmitri
TITLE OF INVENTION: Adenoviral Vectors
FILE REFERENCE: STONYB-04970

CURRENT APPLICATION NUMBER: US/09/782,378A

CURRENT FILING DATE: 2001-02-12

PRIOR FRILMG DATE: 2001-02-12

PRIOR PRILMG DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin version 3.0

SEQ ID NO 4

LENGTH: 35935

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1141 TGARTTTTCTGGCCATGCATCTTTGGAGAGGCGGTTGTGAGACACAAGAATCGCCTGCTAC 1200 	Db Qy	Qy         61 GAGGAGTITGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTAT 120
	Db &	QY 1 ATCGATCTTACCTGCCACGAGGCTTGCCTTTCCACCCAGTGACGACGAGGATGAAGAGGGT 60
	D 4	Query Match 100.0%; Score 2594; DB 9; Length 35935; Best Local Similarity 100.0%; Pred. No. 0; Matches 2594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	S B S	V 5 2
901 CCCAGGCAAAGTTAGTCTGCAGAATTAAGGAGGATTACAAGTGGGAATTTGAAGAGCTTT 960 	gg Qy	R FILING DATE: 2000-10-02  WER OF SEQ ID NOS: 27  WARE: Patentin version 3.0  D NO 5
841 ACTTGCTGGAACAGAGCTCTAACAGTACCTCTTGGTTTTGGAGGTTTCTGTGGGGCTCAT 900	Qy db	R APPLICATION NUMBER: 60/23 R APPLICATION NUMBER: 0S/
781 TGGTTACATCTGACCTCATGGAGGCTTGGGAGGTGTTTGGAAGATTTTTCTGCTGTGCGTA 840	Оу	APPLICANT: Bahou, Wadie  APPLICANT: Sandalon, Ziv  APPLICANT: Gnatenko, Dmitri  TITLE OF INVENTION Adenviral Vectors
721 TGCATGGCGTGTTAAATGGGGCGGGGCTTAAAAGGGTATATAATGCGCCGTGGGCTAATCT 780	Qy Db	; Sequence 5, Application US/09782378A ; Patent No. US20020102731A1 ; GENERAL INFORMATION:
661 CGCCTTTGTTTGCTGAATGAGTTGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACT 720 	D Qy	14 82-378b-5
1517 ACTTGAGCTGTAAACGCCCCAGGCCATAAGGTGTAAACCTGTGATTGCGTGTGTGGGTTAA 1576	Db CY	Qy 2581 AGATACAGATTGAG 2594 
GGCGTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGG	Db .	QY 2521 GCTGAGGCCCGATCACTTGGTGCTGCCTGCACCCGCGCTGAGTTTGGCTCTAGCGATGA 2580
	Q Db	QY 2461 CTGCGAGTGTGGCGGTAAACATATTAGGAACCAGCCTGTGATGCTGGATGTGACCGAGGA 2520
1337 TGTCTAGAGAATACAACACCTC 1396 481 CTGAGATACACACCCGGTGGTCCCCCCTTGTGAACACCACCTC 540	оь	2401 CATGACCATGAAGATCTGGAAGGTGCTGAGGTACGATGAGACCGCCACCAGGTGCAGACC
TGTCTAGAGAATGCAATAGTAGGACGGGTAGCTGTGACTCCGGTCCTTCTAACACACCTC	Q B s	Qy 2341 CACTAAGATATTGCTTGAGCCCGAGAGCATGTCCAAGGTGAACCTGAACGGGTGTTTGA 2400
AAGACCTACCCCCCCTAAAATGGCCCCTGACTATCCTGAGACCCCGACACATCACCTG	Q D \$	Qy 2281 TTCCTTGCATTTGGGTAACAGGAGGGGGGTGTTCCTACCTA
	S B 7	Qy 2221 CGTAGCCAGCCACTCTCGCAAGGCCTGGCCAGTGTTTGAGCATAACATACTGACCGGCTG 2280
	S D 1	Qy 2161 CAGGGCCTCTCAGATGCTGACCTGCTCGGACGGCAACTGTCACCTGCTGAAGACCATTCA 2220
	S B	Qy 2101 CATGCTAGTGAAAAGCGTGGCTGTGATTAAGCATAACATGGTATGTGGCAACTGCGAGGA 2160
121 CACCGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGT 180	δ	Db 2957 TATCCTGTCTGAGGGTAACTCCAGGGTGCGCCACAATGTGGCCTCCGACTGTGGTTGCTT 3016

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TTCCTTGCATTTGGGTAACAGGAGGGGGGTGTTCCTACCTTACCAATGCAATTTGAGTCA 2340
                                                                                                                                                                                                   CAGGGCCTCTCAGATGCTGACCTGCTCGGACGGCAACTGTCACCTTGCTGAAGACCATTCA 2220
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                                                                                     CGTAGCCAGCCACTCTCGCAAGGCCTGGCCAGTGTTTTGAGCATAACATACTGACCCGCTG
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TOPOLOGY: linear;
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MOLECULE TYPE: DNA (genomic);
SEQUENCE DESCRIPTION: SEQ ID
US-09-739-007-43
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Query Match 100.0%; Score 2594; Best Local Similarity 100.0%; Pred. No. 0; Matches 2594; Conservative 0; Mismatches
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Publication No. US20030170885A1
GENERAL INFORMATION:
                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 029395-002
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/379,452
FILING DATE: «Unknown»
APPLICATION NUMBER: FR 93 06482
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Dadio, Susan M.
REGISTRATION NUMBER: 40,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:

CARDARESSEE: BURNS, DOANE, SW
STREET: 1737 King Street, S
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22314-2756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: IMLER, Jean-Luc
MEHTALI, Majid
PAVIRAUI, Andrea
TITLE OF INVENTION: DEPECTIVE ADENOVIRUSES AND CORRESPONDING
COMPLEMENTATION LINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2401
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                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 43
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/739,007 FILING DATE: 19-Dec-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTGAGGCCCGATCACTTGGTGCTGGCCTGCACCCGCGCTGAGTTTGGCTCTAGCGATGA 2580
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                                                                                      NO:
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TRCHAGAGATGGGCCAGAGGGCTAAAAGGGGGTAAAGAGGGAGCGGGGGGCTTGTTGAGGCTACTAAAGAGGATGGGCAAAATCTTATTTCAACAAATCCAACATTAACAACTACTA	1081 TTTTGAGTTTTATAAAGGATAAATGGAGCGAAGAAGAACCCATCTGAGCGGGGGGGG

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Db 3077 CAGGCCTCTCAGATGCTGACCTGCTCGGACGGCAACTGTCACCTCAGATGCTGACCTGCTCGGACGGCAACTGTCACCTAACTGTCACCTAACTGTCACCTAACTGTCACCTAACTGTCACCTAACTGTCACCTAACTGTCACCTAACTGTCACCTAACTGTCACCTAACTGTCACCTAACACTACCTTAACACTAACACTACCTAACATATTGCTTCAACACTACCTAACACTACCTAACATATTGCTTCAACACTACCTAACACCTCAACATAATTGCTTCGAACACTGTCCAAAGATACCTCAACATATTGCTTCGAACACTGTCCAAAGATCCTCAACATATTGCTTCGAACACTGTCCAAAGATCCTCAACATAACATATTAAGAACCATCAACACCTCCAACACTACCTAACACCTCTAACAAC	 AGATGCTGACA ACTCTCGCAAA ACTCTCGCAAA TGGGTAACAG            TGCTTGAGCC            TGCTTGAGCC TGCTTGAGCC AGATCTGGAAA AGATCTGGAAA AGATCTGGAAA AGATCTTGGTAAACA BGGGGTAAACA BGGGGGTAAACA BGGGGGTAAACA BGGGGGTAAACA BGGGGTAAACA BGGGGGTAAACA BGGGGTAAACA BGGGGGTAAACA BGGGGGGGGGGTAAACA BGGGGGGGGGGGGGGA BGGGGGGGGGGGGGGA BGGGGGGGGGG
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